



SEQUENCE LISTING

2110> Steinbuchel, Alexander
 Priefert, Horst
 Rabenhorst, Jorgen

<120> SYNTHETIC ENZYMES FOR THE PRODUCTION OF CONIFERYL
 ALCOHOL, CONIFERYLALDEHYDE, FERULIC ACID, VANILLIN AND
 VANILLIC ACID AND THEIR USE

<130> Bayer-9998-CAO

<140> 09/750,986

<141> 2000-12-28

<150> 196 49 655.1 GERMANY

<151> 1996-11-29

<160> 45

<170> PatentIn Ver. 2.1

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<211> 284

<212> PRT

<213> *Pseudomonas* sp.

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Arg	Asp	Pro	Asn	Lys	Ala	Gly	Asp	Leu	Thr	Ala	Arg	Gly	Ile	Val	Val
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Thr	Ala	Gln	His	Arg	Ala	Val	Ile	Asp	Ala	Ala	Lys	Gln	Glu	Gly	Ile
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Glu	Leu	Leu	Ala	Tyr	Thr	Ser	Leu	Leu	His	Ala	Asp	Lys	Ser	Ala	Leu
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Gly Leu Ala Thr Glu His Arg Asp Thr Glu Gln Ala Leu Thr Glu Ser
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 Gly Ile Pro His Val Leu Leu Arg Asn Gly Trp Tyr His Glu Asn Tyr
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 Val Ala Pro Gln Ala Gly Lys Thr Val Val Tyr Ser Asn Leu Ser Glu
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 Ser Asp Tyr Arg Ser Ala Leu Ile Ser Ala Gly Leu Pro Asp Gly Phe
 225 230 235 240
 Ala Ala Leu Leu Ala Asp Ser Asp Ala Gly Ala Ala Lys Gly Tyr Leu
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 <222> (1)..(1062)
 <223> product = "Vanillinsaeure-O-Demethylase" / gene =
 "vanA"

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 Ala Asp Lys Pro Leu Gly Arg Gln Ile Cys Asn Glu Lys Ile Val Phe
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tat cgg ggg ccg gaa gga cgt gtt gcc gcg gta gag gat ttc tgc cct	144
Tyr Arg Gly Pro Glu Gly Arg Val Ala Ala Val Glu Asp Phe Cys Pro	
35 40 45	
cat cgc ggg gca ccg ttg tcc ctg ggt ttc gtt cgc gac ggt aag ctg	192
His Arg Gly Ala Pro Leu Ser Leu Gly Phe Val Arg Asp Gly Lys Leu	
50 55 60	
att tgc ggc tac cac ggt ttg gaa atg ggc tgc gag ggc aaa acg ctc	240
Ile Cys Gly Tyr His Gly Leu Glu Met Gly Cys Glu Gly Lys Thr Leu	
65 70 75 80	
gcg atg ccc ggg cag cgc gtt caa ggc ttc cct tgc atc aaa agc tac	288
Ala Met Pro Gly Gln Arg Val Gln Gly Phe Pro Cys Ile Lys Ser Tyr	
85 90 95	
gcg gta gaa gag cga tac ggc ttt atc tgg gta tgg cct ggt gat cgc	336
Ala Val Glu Glu Arg Tyr Gly Phe Ile Trp Val Trp Pro Gly Asp Arg	
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gag ctg gcg gat ccg gcg ctt att cac cac ctg gag tgg gcc gat aat	384
Glu Leu Ala Asp Pro Ala Leu Ile His His Leu Glu Trp Ala Asp Asn	
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ccg gag tgg gcc tat ggt ggc ggt ctc tac cac atc gct tgt gat tac	432
Pro Glu Trp Ala Tyr Gly Gly Gly Leu Tyr His Ile Ala Cys Asp Tyr	
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cgc ctg atg atc gac aac ctc atg gat ctc acc cat gag acc tat gtg	480
Arg Leu Met Ile Asp Asn Leu Met Asp Leu Thr His Glu Thr Tyr Val	
145 150 155 160	
cat gcc tcc agc atc ggt caa aag gaa att gac gag gca ccg gtc agt	528
His Ala Ser Ser Ile Gly Gln Lys Glu Ile Asp Glu Ala Pro Val Ser	
165 170 175	
act cgt gtc gag ggc gac acc gtg att acc agc cgg tac atg gat aac	576
Thr Arg Val Glu Gly Asp Thr Val Ile Thr Ser Arg Tyr Met Asp Asn	
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gtc atg gcc cct ccg ttc tgg cgt gct gcg ctt cgt ggc aac ggc ttg	624
Val Met Ala Pro Pro Phe Trp Arg Ala Ala Leu Arg Gly Asn Gly Leu	
195 200 205	
gcc gac gat gta ccg gtt gat cgc tgg cag atc tgc cga ttc gct cct	672
Ala Asp Asp Val Pro Val Asp Arg Trp Gln Ile Cys Arg Phe Ala Pro	
210 215 220	
ccg agt cac gta ctg atc gaa gta ggt gtg gct cat gcg ggc aaa ggc	720
Pro Ser His Val Leu Ile Glu Val Gly Val Ala His Ala Gly Lys Gly	
225 230 235 240	
gga tat gac gcg ccg gcg gaa tac aag gcc ggc agc ata gtg gtc gac	768
Gly Tyr Asp Ala Pro Ala Glu Tyr Lys Ala Gly Ser Ile Val Val Asp	
245 250 255	

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Phe Ile Thr Pro Glu Ser Asp Thr Ser Ile Trp Tyr Phe Trp Gly Met	
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Ala Arg Asn Phe Arg Pro Gln Gly Thr Glu Leu Thr Glu Thr Ile Arg	
275 280 285	
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Val Gly Gln Gly Lys Ile Phe Ala Glu Asp Leu Asp Met Leu Glu Gln	
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Gln Gln Arg Asn Leu Leu Ala Tyr Pro Glu Arg Gln Leu Leu Lys Leu	
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Asn Ile Asp Ala Gly Gly Val Gln Ser Arg Arg Val Ile Asp Arg Ile	
325 330 335	
ctc gca gct gaa caa gag gcc gca gac gca gcg ctg atc gcg aga agt	1056
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 <212> PRT
 <213> Pseudomonas sp.

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Ile Cys Gly Tyr His Gly Leu Glu Met Gly Cys Glu Gly Lys Thr Leu	
65 70 75 80	
Ala Met Pro Gly Gln Arg Val Gln Gly Phe Pro Cys Ile Lys Ser Tyr	
85 90 95	
Ala Val Glu Glu Arg Tyr Gly Phe Ile Trp Val Trp Pro Gly Asp Arg	
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Glu	Leu	Ala	Asp	Pro	Ala	Leu	Ile	His	His	Leu	Glu	Trp	Ala	Asp	Asn	115	120	125
Pro	Glu	Trp	Ala	Tyr	Gly	Gly	Gly	Leu	Tyr	His	Ile	Ala	Cys	Asp	Tyr	130	135	140
Arg	Leu	Met	Ile	Asp	Asn	Leu	Met	Asp	Leu	Thr	His	Glu	Thr	Tyr	Val	145	150	155
His	Ala	Ser	Ser	Ile	Gly	Gln	Lys	Glu	Ile	Asp	Glu	Ala	Pro	Val	Ser	165	170	175
Thr	Arg	Val	Glu	Gly	Asp	Thr	Val	Ile	Thr	Ser	Arg	Tyr	Met	Asp	Asn	180	185	190
Val	Met	Ala	Pro	Pro	Phe	Trp	Arg	Ala	Ala	Leu	Arg	Gly	Asn	Gly	Leu	195	200	205
Ala	Asp	Asp	Val	Pro	Val	Asp	Arg	Trp	Gln	Ile	Cys	Arg	Phe	Ala	Pro	210	215	220
Pro	Ser	His	Val	Leu	Ile	Glu	Val	Gly	Val	Ala	His	Ala	Gly	Lys	Gly	225	230	235
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Gln	Gln	Arg	Asn	Leu	Leu	Ala	Tyr	Pro	Glu	Arg	Gln	Leu	Leu	Lys	Leu	305	310	315
Asn	Ile	Asp	Ala	Gly	Gly	Val	Gln	Ser	Arg	Arg	Val	Ile	Asp	Arg	Ile	325	330	335
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<211> 954

<212> DNA

<213> Pseudomonas sp.

<220>

<221> CDS

<222> (1)..(951)

<223> product = "Vanillin-O-Demethylase"/ gene = "vanB"

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Ile Ser Leu Glu Phe Val Arg Ala Asp Gly Gly Leu Leu Pro Pro Val	
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gag gcc ggc gcc cac gtc gat gtg cat ctt cct ggc ggc ctg att cgg	144
Glu Ala Gly Ala His Val Asp Val His Leu Pro Gly Gly Leu Ile Arg	
35 40 45	
cag tac tcg ctc tgg aat caa cca ggg gcg cag agc cat tac tgc atc	192
Gln Tyr Ser Leu Trp Asn Gln Pro Gly Ala Gln Ser His Tyr Cys Ile	
50 55 60	
ggt gtt ctg aag gac ccg gcg tct cgt ggt ggt tcg aag gcg gtg cac	240
Gly Val Leu Lys Asp Pro Ala Ser Arg Gly Gly Ser Lys Ala Val His	
65 70 75 80	
gag aat ctt cgc gtc ggg atg cgc gtg caa att agc gag ccg agg aac	288
Glu Asn Leu Arg Val Gly Met Arg Val Gln Ile Ser Glu Pro Arg Asn	
85 90 95	
cta ttc cca ttg gaa gag ggg gtg gag cgg agt ctg ctg ttc gcg ggc	336
Leu Phe Pro Leu Glu Glu Gly Val Glu Arg Ser Leu Leu Phe Ala Gly	
100 105 110	
ggg att ggc att acg ccg att ctg tgt atg gct caa gaa tta gca gca	384
Gly Ile Gly Ile Thr Pro Ile Leu Cys Met Ala Gln Glu Leu Ala Ala	
115 120 125	
cgc gag caa gat ttc gag ttg cat tat tgc gcg cgt tcg acc gac cga	432
Arg Glu Gln Asp Phe Glu Leu His Tyr Cys Ala Arg Ser Thr Asp Arg	
130 135 140	
gcg gcg ttc gtt gaa tgg ctt aag gtt tgc gac ttt gct gat cac gta	480
Ala Ala Phe Val Glu Trp Leu Lys Val Cys Asp Phe Ala Asp His Val	
145 150 155 160	
cgt ttc cac ttt gac aat ggc ccg gat cag caa aaa ctg aat gcc gca	528
Arg Phe His Phe Asp Asn Gly Pro Asp Gln Gln Lys Leu Asn Ala Ala	
165 170 175	
gcg ctg cta gcg gcc gag gcc gaa ggt acc cac ctt tat gtc tgt ggg	576
Ala Leu Leu Ala Ala Glu Ala Glu Gly Thr His Leu Tyr Val Cys Gly	
180 185 190	
ccc ggc ggg ttc atg ggg cat gtg ctt gat acc gcg aag gag cag ggc	624
Pro Gly Gly Phe Met Gly His Val Leu Asp Thr Ala Lys Glu Gln Gly	
195 200 205	
tgg gct gac aat cga ctg cat cga gag tat ttc gcc gcg gcg ccg aat	672

Trp	Ala	Asp	Asn	Arg	Leu	His	Arg	Glu	Tyr	Phe	Ala	Ala	Ala	Pro	Asn		
210						215					220						
gtg	agt	gct	gac	gat	ggc	agt	ttc	gag	gtg	cgg	att	cac	agc	acc	gga	720	
Val	Ser	Ala	Asp	Asp	Gly	Ser	Phe	Glu	Val	Arg	Ile	His	Ser	Thr	Gly		
225					230					235					240		
caa	gtg	ctt	cag	gtc	ccc	gcg	gat	caa	acg	gtc	tcc	cag	gtg	ctc	gat	768	
Gln	Val	Leu	Gln	Val	Pro	Ala	Asp	Gln	Thr	Val	Ser	Gln	Val	Leu	Asp		
				245					250					255			
gcg	gcc	gga	att	atc	gtt	ccc	gtt	tct	tgt	gag	cag	ggc	atc	tgc	ggg	816	
Ala	Ala	Gly	Ile	Ile	Val	Pro	Val	Ser	Cys	Glu	Gln	Gly	Ile	Cys	Gly		
			260					265					270				
act	tgc	atc	act	cgg	gtg	gta	gac	gga	gag	cct	gat	cat	cgt	gac	ttc	864	
Thr	Cys	Ile	Thr	Arg	Val	Val	Asp	Gly	Glu	Pro	Asp	His	Arg	Asp	Phe		
		275					280					285					
ttc	ctc	acg	gat	gcg	gag	aag	gca	aag	aac	gac	cag	ttc	acc	ccc	tgt	912	
Phe	Leu	Thr	Asp	Ala	Glu	Lys	Ala	Lys	Asn	Asp	Gln	Phe	Thr	Pro	Cys		
	290					295					300						
tgc	tcg	cga	gcc	aag	agc	gcc	tgt	ttg	gtc	ttg	gat	ctc	taa			954	
Cys	Ser	Arg	Ala	Lys	Ser	Ala	Cys	Leu	Val	Leu	Asp	Leu					
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			20					25					30				
Glu	Ala	Gly	Ala	His	Val	Asp	Val	His	Leu	Pro	Gly	Gly	Leu	Ile	Arg		
		35					40					45					
Gln	Tyr	Ser	Leu	Trp	Asn	Gln	Pro	Gly	Ala	Gln	Ser	His	Tyr	Cys	Ile		
	50				55						60						
Gly	Val	Leu	Lys	Asp	Pro	Ala	Ser	Arg	Gly	Gly	Ser	Lys	Ala	Val	His		
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Glu	Asn	Leu	Arg	Val	Gly	Met	Arg	Val	Gln	Ile	Ser	Glu	Pro	Arg	Asn		
			85						90					95			
Leu	Phe	Pro	Leu	Glu	Glu	Gly	Val	Glu	Arg	Ser	Leu	Leu	Phe	Ala	Gly		
		100						105					110				
Gly	Ile	Gly	Ile	Thr	Pro	Ile	Leu	Cys	Met	Ala	Gln	Glu	Leu	Ala	Ala		
	115						120					125					

Arg Glu Gln Asp Phe Glu Leu His Tyr Cys Ala Arg Ser Thr Asp Arg
 130 135 140
 Ala Ala Phe Val Glu Trp Leu Lys Val Cys Asp Phe Ala Asp His Val
 145 150 155 160
 Arg Phe His Phe Asp Asn Gly Pro Asp Gln Gln Lys Leu Asn Ala Ala
 165 170 175
 Ala Leu Leu Ala Ala Glu Ala Glu Gly Thr His Leu Tyr Val Cys Gly
 180 185 190
 Pro Gly Gly Phe Met Gly His Val Leu Asp Thr Ala Lys Glu Gln Gly
 195 200 205
 Trp Ala Asp Asn Arg Leu His Arg Glu Tyr Phe Ala Ala Ala Pro Asn
 210 215 220
 Val Ser Ala Asp Asp Gly Ser Phe Glu Val Arg Ile His Ser Thr Gly
 225 230 235 240
 Gln Val Leu Gln Val Pro Ala Asp Gln Thr Val Ser Gln Val Leu Asp
 245 250 255
 Ala Ala Gly Ile Ile Val Pro Val Ser Cys Glu Gln Gly Ile Cys Gly
 260 265 270
 Thr Cys Ile Thr Arg Val Val Asp Gly Glu Pro Asp His Arg Asp Phe
 275 280 285
 Phe Leu Thr Asp Ala Glu Lys Ala Lys Asn Asp Gln Phe Thr Pro Cys
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 Cys Ser Arg Ala Lys Ser Ala Cys Leu Val Leu Asp Leu
 305 310 315

<210> 7

<211> 1119

<212> DNA

<213> Pseudomonas sp.

<220>

<221> CDS

<222> (1)..(1116)

<223> product = "Formaldehyd-Dehydrogenase"/ gene =
 "fdh"

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cag atc gtc gaa gtg gac gtg gct ccg ccc aag gcc ggt gaa gtc ctg	96
Gln Ile Val Glu Val Asp Val Ala Pro Pro Lys Ala Gly Glu Val Leu	
20 25 30	
gtg cgg gtc gtg gcc acc ggc gtt tgc cac acc gat gcc tac acc ctg	144
Val Arg Val Val Ala Thr Gly Val Cys His Thr Asp Ala Tyr Thr Leu	
35 40 45	
tcc ggc gct gat tcc gag ggc gtt ttc ccc tgc atc ctt ggt cac gaa	192
Ser Gly Ala Asp Ser Glu Gly Val Phe Pro Cys Ile Leu Gly His Glu	
50 55 60	
ggc ggc ggc att gtc gaa gcg gtg ggc gag ggc gtc acc tcg ctg gcg	240
Gly Gly Gly Ile Val Glu Ala Val Gly Glu Gly Val Thr Ser Leu Ala	
65 70 75 80	
gtc ggc gac cac gtg atc ccg ctc tac acg gcc gaa tgc cgt gag tgc	288
Val Gly Asp His Val Ile Pro Leu Tyr Thr Ala Glu Cys Arg Glu Cys	
85 90 95	
aag ttc ttc aag tcc ggc aag acc aac ctg tgc cag aaa gtg cgt gct	336
Lys Phe Phe Lys Ser Gly Lys Thr Asn Leu Cys Gln Lys Val Arg Ala	
100 105 110	
act cag ggc aag ggt ctg atg ccg gac ggc acc tcc cgc ttc agc tac	384
Thr Gln Gly Lys Gly Leu Met Pro Asp Gly Thr Ser Arg Phe Ser Tyr	
115 120 125	
aac ggt cag ccg atc tac cac tac atg ggc tgc tcg acc ttc tcc gag	432
Asn Gly Gln Pro Ile Tyr His Tyr Met Gly Cys Ser Thr Phe Ser Glu	
130 135 140	
tac acc gtg ctg ccg gaa atc tcc ctg gcg aag att ccc aag aat gcg	480
Tyr Thr Val Leu Pro Glu Ile Ser Leu Ala Lys Ile Pro Lys Asn Ala	
145 150 155 160	
ccg ctg gag aaa gtc tgc ctg ctg ggc tgc ggc gtg acc acc ggc att	528
Pro Leu Glu Lys Val Cys Leu Leu Gly Cys Gly Val Thr Thr Gly Ile	
165 170 175	
ggc gcg gtg ctg aac act gcc aag gtg gag gag ggt gct acc gtg gcc	576
Gly Ala Val Leu Asn Thr Ala Lys Val Glu Glu Gly Ala Thr Val Ala	
180 185 190	
atc ttc ggc ctg ggc ggc atc ggc ttg gcg gcg atc atc ggc gcg aag	624
Ile Phe Gly Leu Gly Gly Ile Gly Leu Ala Ala Ile Ile Gly Ala Lys	
195 200 205	
atg gcc aag gcc tcg cgc atc atc gcc atc gac atc aat ccg tcc aag	672
Met Ala Lys Ala Ser Arg Ile Ile Ala Ile Asp Ile Asn Pro Ser Lys	
210 215 220	
ttc gat gtg gct cgc gag ctg ggc gcc act gac ttc gtc aat ccg aac	720
Phe Asp Val Ala Arg Glu Leu Gly Ala Thr Asp Phe Val Asn Pro Asn	
225 230 235 240	
gat cac gcg aag ccg atc cag gat gtc atc gtc gag atg act gat ggc	768

Asp	His	Ala	Lys	Pro	Ile	Gln	Asp	Val	Ile	Val	Glu	Met	Thr	Asp	Gly		
				245					250						255		
ggg	gtg	gac	tac	agc	ttc	gag	tgc	atc	ggc	aac	gtt	cga	ctc	atg	cgc	816	
Gly	Val	Asp	Tyr	Ser	Phe	Glu	Cys	Ile	Gly	Asn	Val	Arg	Leu	Met	Arg		
			260					265					270				
gca	gca	ctc	gag	tgc	tgc	cac	aag	ggc	tgg	ggc	gaa	tcc	gtg	atc	atc	864	
Ala	Ala	Leu	Glu	Cys	Cys	His	Lys	Gly	Trp	Gly	Glu	Ser	Val	Ile	Ile		
		275					280					285					
ggc	gtg	gcg	ccg	gcg	ggg	gcc	gaa	atc	aac	acc	cgt	ccg	ttc	cac	ctg	912	
Gly	Val	Ala	Pro	Ala	Gly	Ala	Glu	Ile	Asn	Thr	Arg	Pro	Phe	His	Leu		
	290					295					300						
gtg	acc	ggg	cgc	gtc	tgg	cgg	ggg	tcg	gcg	ttc	ggg	gta	aag	ggc		960	
Val	Thr	Gly	Arg	Val	Trp	Arg	Gly	Ser	Ala	Phe	Gly	Gly	Val	Lys	Gly		
305					310					315				320			
cgc	acc	gaa	ctg	ccg	agc	tac	gtg	gag	aag	gca	cag	cag	ggc	gag	atc	1008	
Arg	Thr	Glu	Leu	Pro	Ser	Tyr	Val	Glu	Lys	Ala	Gln	Gln	Gly	Glu	Ile		
				325					330					335			
ccg	ctg	gac	acc	ttc	atc	act	cac	acc	atg	ggc	ctg	gac	gac	atc	aac	1056	
Pro	Leu	Asp	Thr	Phe	Ile	Thr	His	Thr	Met	Gly	Leu	Asp	Asp	Ile	Asn		
			340					345					350				
acg	gcc	ttc	gac	ctg	atg	gac	gaa	ggg	aag	agc	atc	cgc	tct	gtt	gtt	1104	
Thr	Ala	Phe	Asp	Leu	Met	Asp	Glu	Gly	Lys	Ser	Ile	Arg	Ser	Val	Val		
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caa	ttg	agt	cgc	tag												1119	
Gln	Leu	Ser	Arg														
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		20					25						30			
Val	Arg	Val	Val	Ala	Thr	Gly	Val	Cys	His	Thr	Asp	Ala	Tyr	Thr	Leu	
		35				40					45					
Ser	Gly	Ala	Asp	Ser	Glu	Gly	Val	Phe	Pro	Cys	Ile	Leu	Gly	His	Glu	
	50					55					60					
Gly	Gly	Gly	Ile	Val	Glu	Ala	Val	Gly	Glu	Gly	Val	Thr	Ser	Leu	Ala	
65					70				75						80	

Val	Gly	Asp	His	Val	Ile	Pro	Leu	Tyr	Thr	Ala	Glu	Cys	Arg	Glu	Cys	
				85					90					95		
Lys	Phe	Phe	Lys	Ser	Gly	Lys	Thr	Asn	Leu	Cys	Gln	Lys	Val	Arg	Ala	
				100					105					110		
Thr	Gln	Gly	Lys	Gly	Leu	Met	Pro	Asp	Gly	Thr	Ser	Arg	Phe	Ser	Tyr	
				115					120					125		
Asn	Gly	Gln	Pro	Ile	Tyr	His	Tyr	Met	Gly	Cys	Ser	Thr	Phe	Ser	Glu	
				130					135					140		
Tyr	Thr	Val	Leu	Pro	Glu	Ile	Ser	Leu	Ala	Lys	Ile	Pro	Lys	Asn	Ala	
				145					150					155		
Pro	Leu	Glu	Lys	Val	Cys	Leu	Leu	Gly	Cys	Gly	Val	Thr	Thr	Gly	Ile	
				165					170					175		
Gly	Ala	Val	Leu	Asn	Thr	Ala	Lys	Val	Glu	Glu	Gly	Ala	Thr	Val	Ala	
				180					185					190		
Ile	Phe	Gly	Leu	Gly	Gly	Ile	Gly	Leu	Ala	Ala	Ile	Ile	Gly	Ala	Lys	
				195					200					205		
Met	Ala	Lys	Ala	Ser	Arg	Ile	Ile	Ala	Ile	Asp	Ile	Asn	Pro	Ser	Lys	
				210					215					220		
Phe	Asp	Val	Ala	Arg	Glu	Leu	Gly	Ala	Thr	Asp	Phe	Val	Asn	Pro	Asn	
				225					230					235		
Asp	His	Ala	Lys	Pro	Ile	Gln	Asp	Val	Ile	Val	Glu	Met	Thr	Asp	Gly	
				245					250					255		
Gly	Val	Asp	Tyr	Ser	Phe	Glu	Cys	Ile	Gly	Asn	Val	Arg	Leu	Met	Arg	
				260					265					270		
Ala	Ala	Leu	Glu	Cys	Cys	His	Lys	Gly	Trp	Gly	Glu	Ser	Val	Ile	Ile	
				275					280					285		
Gly	Val	Ala	Pro	Ala	Gly	Ala	Glu	Ile	Asn	Thr	Arg	Pro	Phe	His	Leu	
				290					295					300		
Val	Thr	Gly	Arg	Val	Trp	Arg	Gly	Ser	Ala	Phe	Gly	Gly	Val	Lys	Gly	
				305					310					315		
Arg	Thr	Glu	Leu	Pro	Ser	Tyr	Val	Glu	Lys	Ala	Gln	Gln	Gly	Glu	Ile	
				325					330					335		
Pro	Leu	Asp	Thr	Phe	Ile	Thr	His	Thr	Met	Gly	Leu	Asp	Asp	Ile	Asn	
				340					345					350		
Thr	Ala	Phe	Asp	Leu	Met	Asp	Glu	Gly	Lys	Ser	Ile	Arg	Ser	Val	Val	
				355					360					365		
Gln	Leu	Ser	Arg													
				370												

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 <211> 1638
 <212> DNA
 <213> Pseudomonas sp.

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 <222> (1)..(1635)
 <223> product = "gamma-Glutamylcystein-Synthetase" /
 gene = "gcs"

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 Met Pro Gln Thr Leu Ala Gly Arg Leu Ser Leu Leu Ser Gly Thr Asp
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 gaa tta acc ctg ctt ctt cgg ggt ggt cgg ggc att gag cgt gaa gcc 96
 Glu Leu Thr Leu Leu Leu Arg Gly Gly Arg Gly Ile Glu Arg Glu Ala
 20 25 30
 ttg cgg gtc gat gtt caa ggt gaa ctg gcg ctg acg cct cac ccg gcg 144
 Leu Arg Val Asp Val Gln Gly Glu Leu Ala Leu Thr Pro His Pro Ala
 35 40 45
 gcg ctt ggc tct gcg ttg acc cat ccg aca att act acg gat tac gcc 192
 Ala Leu Gly Ser Ala Leu Thr His Pro Thr Ile Thr Thr Asp Tyr Ala
 50 55 60
 gag gcc ctg ctt gag ttg atc act cgg ccg gca acc gat tgt gcg caa 240
 Glu Ala Leu Leu Glu Leu Ile Thr Arg Pro Ala Thr Asp Cys Ala Gln
 65 70 75 80
 gcc ttg gct gag ctg gag gag ctt cac cgt ttc gtt cat tcg aga ctt 288
 Ala Leu Ala Glu Leu Glu Glu Leu His Arg Phe Val His Ser Arg Leu
 85 90 95
 gag ggg gag tat ctc tgg aat ctg tcc atg cct ggc aga ttg ccg gtt 336
 Glu Gly Glu Tyr Leu Trp Asn Leu Ser Met Pro Gly Arg Leu Pro Val
 100 105 110
 gat gag caa atc ccg att gct tgg tat gga cca tca aat cca ggc atg 384
 Asp Glu Gln Ile Pro Ile Ala Trp Tyr Gly Pro Ser Asn Pro Gly Met
 115 120 125
 ttg cgc cac gtt tat cgc cgt ggc cta gct ctg cgt tat ggc aag cga 432
 Leu Arg His Val Tyr Arg Arg Gly Leu Ala Leu Arg Tyr Gly Lys Arg
 130 135 140
 atg caa tgc atc gca ggg att cac tac aac tac tca ctg ccg cca gag 480
 Met Gln Cys Ile Ala Gly Ile His Tyr Asn Tyr Ser Leu Pro Pro Glu
 145 150 155 160
 ctt ttc gct gtc ctg acc aag gca gag gtc ggg tct ccc aag tta ctg 528

Leu Phe Ala Val Leu Thr Lys Ala Glu Val Gly Ser Pro Lys Leu Leu
165 170 175

gag cgc cag tca gca gct tac atg cgc caa att cgc aac ctt cgg caa 576
Glu Arg Gln Ser Ala Ala Tyr Met Arg Gln Ile Arg Asn Leu Arg Gln
180 185 190

tac ggt tgg ttg ctg gcc tac ttg ttc ggc gct tcc ccc gcc atc tgc 624
Tyr Gly Trp Leu Leu Ala Tyr Leu Phe Gly Ala Ser Pro Ala Ile Cys
195 200 205

aag agc ttc ttg ggg ggc gag aga gat gag cta gct cgc atg ggg ggc 672
Lys Ser Phe Leu Gly Gly Glu Arg Asp Glu Leu Ala Arg Met Gly Gly
210 215 220

gat acg ctt tac atg ccc tat gca acc agc ttg cgc atg agt gac atc 720
Asp Thr Leu Tyr Met Pro Tyr Ala Thr Ser Leu Arg Met Ser Asp Ile
225 230 235 240

ggg tac cgc aac cgt gcc atg gat gat cta tct ccc agc ctg aat gat 768
Gly Tyr Arg Asn Arg Ala Met Asp Asp Leu Ser Pro Ser Leu Asn Asp
245 250 255

ctg ggt gcc tat att cgc gat att tgc cgt gct ctt cac act ccc gat 816
Leu Gly Ala Tyr Ile Arg Asp Ile Cys Arg Ala Leu His Thr Pro Asp
260 265 270

gcc cag tac cag gcg ctg ggt gtg ttt gca cag ggc gag tgg cgg cag 864
Ala Gln Tyr Gln Ala Leu Gly Val Phe Ala Gln Gly Glu Trp Arg Gln
275 280 285

tta aac gcc aat cta ttg cag ttg gat agt gag tac tac gca ctg gcg 912
Leu Asn Ala Asn Leu Leu Gln Leu Asp Ser Glu Tyr Tyr Ala Leu Ala
290 295 300

cga ccg aag tca gcg ccc gag cgg ggg gag cga aac ctg gat gct ctc 960
Arg Pro Lys Ser Ala Pro Glu Arg Gly Glu Arg Asn Leu Asp Ala Leu
305 310 315 320

gct agg cgt gga gtc cag tat gtg gag ctg cgc gca ctg gat ctc gat 1008
Ala Arg Arg Gly Val Gln Tyr Val Glu Leu Arg Ala Leu Asp Leu Asp
325 330 335

cca ttc tcc ccg tta ggc att ggc ctg acc tgc gcc aag ttc ctc gat 1056
Pro Phe Ser Pro Leu Gly Ile Gly Leu Thr Cys Ala Lys Phe Leu Asp
340 345 350

ggc ttt ttg ctt ttc tgc ttg ttg tct gag gcg ccg gtt gat gat cga 1104
Gly Phe Leu Leu Phe Cys Leu Leu Ser Glu Ala Pro Val Asp Asp Arg
355 360 365

aat gcc cag cgt tca aga ccg gga aaa tct gag cct ggc cgg caa gta 1152
Asn Ala Gln Arg Ser Arg Pro Gly Lys Ser Glu Pro Gly Arg Gln Val
370 375 380

cg	gc	tca	cct	ggc	tta	aag	ctg	cat	cg	aat	gg	cag	tcc	att	ctc	1200
Arg	Ala	Ser	Pro	Gly	Leu	Lys	Leu	His	Arg	Asn	Gly	Gln	Ser	Ile	Leu	
385					390					395					400	

ctc	aag	gat	tgg	gc	cag	gaa	gtg	ttg	acg	gag	gtt	cag	gcc	tgt	gtg	1248
Leu	Lys	Asp	Trp	Ala	Gln	Glu	Val	Leu	Thr	Glu	Val	Gln	Ala	Cys	Val	
				405					410					415		

gaa	ttg	ctc	gac	agt	gca	aat	ggg	ggc	tca	tct	cac	gca	ttg	gct	tgg	1296
Glu	Leu	Leu	Asp	Ser	Ala	Asn	Gly	Gly	Ser	Ser	His	Ala	Leu	Ala	Trp	
			420					425					430			

tca	gca	cag	gag	gaa	aag	gtg	ctt	aat	ccg	gat	tgt	gc	cca	tca	gct	1344
Ser	Ala	Gln	Glu	Glu	Lys	Val	Leu	Asn	Pro	Asp	Cys	Ala	Pro	Ser	Ala	
		435					440					445				

cag	gtg	ctc	gca	gag	ata	cac	aga	cac	gg	ggg	agc	ttc	acg	gca	ttt	1392
Gln	Val	Leu	Ala	Glu	Ile	His	Arg	His	Gly	Gly	Ser	Phe	Thr	Ala	Phe	
	450					455					460					

gg	cgc	caa	tta	gct	atc	gac	cat	gca	aaa	cac	ttc	agt	gcc	tcc	tcg	1440
Gly	Arg	Gln	Leu	Ala	Ile	Asp	His	Ala	Lys	His	Phe	Ser	Ala	Ser	Ser	
465					470					475					480	

ctt	gag	gct	ggc	gta	gcc	aaa	gc	ctt	gac	ctc	cag	gc	acg	tcg	tct	1488
Leu	Glu	Ala	Gly	Val	Ala	Lys	Ala	Leu	Asp	Leu	Gln	Ala	Thr	Ser	Ser	
			485						490					495		

ctg	cgc	gag	cag	cat	caa	ttg	gag	gcc	aac	gac	cgt	gc	cca	ttt	tct	1536
Leu	Arg	Glu	Gln	His	Gln	Leu	Glu	Ala	Asn	Asp	Arg	Ala	Pro	Phe	Ser	
			500					505					510			

gac	tac	ctt	cag	caa	ttc	tcc	ctg	gct	ttc	gg	caa	tcc	gtc	ggc	gcc	1584
Asp	Tyr	Leu	Gln	Gln	Phe	Ser	Leu	Ala	Phe	Gly	Gln	Ser	Val	Gly	Ala	
		515					520					525				

tct	cgt	gc	ccc	aac	cct	acc	gc	cac	ctc	atc	gat	ctg	acc	cct	cct	1632
Ser	Arg	Ala	Pro	Asn	Pro	Thr	Ala	His	Leu	Ile	Asp	Leu	Thr	Pro	Pro	
	530					535					540					

gtc	taa															1638
Val																
545																

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<211> 545

<212> PRT

<213> Pseudomonas sp.

<400> 10

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20	25	30
Leu Arg Val Asp Val Gln Gly Glu Leu Ala Leu Thr Pro His Pro Ala		
35	40	45
Ala Leu Gly Ser Ala Leu Thr His Pro Thr Ile Thr Thr Asp Tyr Ala		
50	55	60
Glu Ala Leu Leu Glu Leu Ile Thr Arg Pro Ala Thr Asp Cys Ala Gln		
65	70	75 80
Ala Leu Ala Glu Leu Glu Glu Leu His Arg Phe Val His Ser Arg Leu		
85	90	95
Glu Gly Glu Tyr Leu Trp Asn Leu Ser Met Pro Gly Arg Leu Pro Val		
100	105	110
Asp Glu Gln Ile Pro Ile Ala Trp Tyr Gly Pro Ser Asn Pro Gly Met		
115	120	125
Leu Arg His Val Tyr Arg Arg Gly Leu Ala Leu Arg Tyr Gly Lys Arg		
130	135	140
Met Gln Cys Ile Ala Gly Ile His Tyr Asn Tyr Ser Leu Pro Pro Glu		
145	150	155 160
Leu Phe Ala Val Leu Thr Lys Ala Glu Val Gly Ser Pro Lys Leu Leu		
165	170	175
Glu Arg Gln Ser Ala Ala Tyr Met Arg Gln Ile Arg Asn Leu Arg Gln		
180	185	190
Tyr Gly Trp Leu Leu Ala Tyr Leu Phe Gly Ala Ser Pro Ala Ile Cys		
195	200	205
Lys Ser Phe Leu Gly Gly Glu Arg Asp Glu Leu Ala Arg Met Gly Gly		
210	215	220
Asp Thr Leu Tyr Met Pro Tyr Ala Thr Ser Leu Arg Met Ser Asp Ile		
225	230	235 240
Gly Tyr Arg Asn Arg Ala Met Asp Asp Leu Ser Pro Ser Leu Asn Asp		
245	250	255
Leu Gly Ala Tyr Ile Arg Asp Ile Cys Arg Ala Leu His Thr Pro Asp		
260	265	270
Ala Gln Tyr Gln Ala Leu Gly Val Phe Ala Gln Gly Glu Trp Arg Gln		
275	280	285
Leu Asn Ala Asn Leu Leu Gln Leu Asp Ser Glu Tyr Tyr Ala Leu Ala		
290	295	300
Arg Pro Lys Ser Ala Pro Glu Arg Gly Glu Arg Asn Leu Asp Ala Leu		
305	310	315 320

Ala Arg Arg Gly Val Gln Tyr Val Glu Leu Arg Ala Leu Asp Leu Asp
 325 330 335
 Pro Phe Ser Pro Leu Gly Ile Gly Leu Thr Cys Ala Lys Phe Leu Asp
 340 345 350
 Gly Phe Leu Leu Phe Cys Leu Leu Ser Glu Ala Pro Val Asp Asp Arg
 355 360 365
 Asn Ala Gln Arg Ser Arg Pro Gly Lys Ser Glu Pro Gly Arg Gln Val
 370 375 380
 Arg Ala Ser Pro Gly Leu Lys Leu His Arg Asn Gly Gln Ser Ile Leu
 385 390 395 400
 Leu Lys Asp Trp Ala Gln Glu Val Leu Thr Glu Val Gln Ala Cys Val
 405 410 415
 Glu Leu Leu Asp Ser Ala Asn Gly Gly Ser Ser His Ala Leu Ala Trp
 420 425 430
 Ser Ala Gln Glu Glu Lys Val Leu Asn Pro Asp Cys Ala Pro Ser Ala
 435 440 445
 Gln Val Leu Ala Glu Ile His Arg His Gly Gly Ser Phe Thr Ala Phe
 450 455 460
 Gly Arg Gln Leu Ala Ile Asp His Ala Lys His Phe Ser Ala Ser Ser
 465 470 475 480
 Leu Glu Ala Gly Val Ala Lys Ala Leu Asp Leu Gln Ala Thr Ser Ser
 485 490 495
 Leu Arg Glu Gln His Gln Leu Glu Ala Asn Asp Arg Ala Pro Phe Ser
 500 505 510
 Asp Tyr Leu Gln Gln Phe Ser Leu Ala Phe Gly Gln Ser Val Gly Ala
 515 520 525
 Ser Arg Ala Pro Asn Pro Thr Ala His Leu Ile Asp Leu Thr Pro Pro
 530 535 540
 Val
 545

<210> 11
 <211> 354
 <212> DNA
 <213> Pseudomonas sp.
 <220>
 <221> CDS
 <222> (1)..(351)
 <223> product = "Cytochrom C UE-Eugenol-Hydroxylase" /

gene = "chyA"

<400> 11

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Met	Met	Asn	Val	Asn	Tyr	Lys	Ala	Val	Gly	Ala	Ser	Leu	Leu	Leu	Ala	
1				5					10						15	

ttc	atc	tct	cag	gga	gct	tgg	gca	gag	agc	ccc	gca	gcc	tct	ggc	aat	96
Phe	Ile	Ser	Gln	Gly	Ala	Trp	Ala	Glu	Ser	Pro	Ala	Ala	Ser	Gly	Asn	
			20					25					30			

acc	cct	gac	att	tat	cga	aag	acc	tgc	acc	tac	tgc	cat	gag	cct	act	144
Thr	Pro	Asp	Ile	Tyr	Arg	Lys	Thr	Cys	Thr	Tyr	Cys	His	Glu	Pro	Thr	
		35					40					45				

gtc	aac	aat	ggc	cgg	gtc	att	gcc	cga	agc	ctc	ggg	ccg	act	ctg	cga	192
Val	Asn	Asn	Gly	Arg	Val	Ile	Ala	Arg	Ser	Leu	Gly	Pro	Thr	Leu	Arg	
	50					55					60					

ggg	cgc	cag	atc	cct	cca	cag	tac	acg	gag	tac	atg	gtg	cgt	cat	gga	240
Gly	Arg	Gln	Ile	Pro	Pro	Gln	Tyr	Thr	Glu	Tyr	Met	Val	Arg	His	Gly	
65					70				75						80	

cgc	ggg	gca	atg	cct	gca	ttc	tct	gaa	gca	gaa	gtg	cct	ccg	gcg	gag	288
Arg	Gly	Ala	Met	Pro	Ala	Phe	Ser	Glu	Ala	Glu	Val	Pro	Pro	Ala	Glu	
			85					90						95		

ctg	aaa	gtt	ctg	ggc	gat	tgg	att	cag	caa	agc	agt	gct	ccc	aaa	gac	336
Leu	Lys	Val	Leu	Gly	Asp	Trp	Ile	Gln	Gln	Ser	Ser	Ala	Pro	Lys	Asp	
			100					105					110			

gct	gga	gtc	gcg	cca	tga											354
Ala	Gly	Val	Ala	Pro												
			115													

<210> 12

<211> 117

<212> PRT

<213> Pseudomonas sp.

<400> 12

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1				5					10						15

Phe	Ile	Ser	Gln	Gly	Ala	Trp	Ala	Glu	Ser	Pro	Ala	Ala	Ser	Gly	Asn
			20					25					30		

Thr	Pro	Asp	Ile	Tyr	Arg	Lys	Thr	Cys	Thr	Tyr	Cys	His	Glu	Pro	Thr
		35					40					45			

Val	Asn	Asn	Gly	Arg	Val	Ile	Ala	Arg	Ser	Leu	Gly	Pro	Thr	Leu	Arg
	50					55					60				

Gly	Arg	Gln	Ile	Pro	Pro	Gln	Tyr	Thr	Glu	Tyr	Met	Val	Arg	His	Gly
65					70				75						80

Arg Gly Ala Met Pro Ala Phe Ser Glu Ala Glu Val Pro Pro Ala Glu
85 90 95

Leu Lys Val Leu Gly Asp Trp Ile Gln Gln Ser Ser Ala Pro Lys Asp
100 105 110

Ala Gly Val Ala Pro
115

<210> 13
<211> 687
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(684)
<223> gene = "ORF5"

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Met Thr Thr Arg Arg Asn Phe Leu Ile Gly Ala Ser Gln Val Gly Ala
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ttg gtg atg atg tcg ccg aaa ttg gtc ttc cgt acg ccg ctc aag cag 96
Leu Val Met Met Ser Pro Lys Leu Val Phe Arg Thr Pro Leu Lys Gln
20 25 30
aag ccc gtg cgc atc ctg tcg acc ggg ctg gcc ggt gag caa gag ttt 144
Lys Pro Val Arg Ile Leu Ser Thr Gly Leu Ala Gly Glu Gln Glu Phe
35 40 45
cac tcg atg ctt cgc gcg cga ttg acc cat acg ggt cag gtc gac atc 192
His Ser Met Leu Arg Ala Arg Leu Thr His Thr Gly Gln Val Asp Ile
50 55 60
gcg tcg gta ccg ctg gac gca gct att tgg gct tct ccc gct cga ctt 240
Ala Ser Val Pro Leu Asp Ala Ala Ile Trp Ala Ser Pro Ala Arg Leu
65 70 75 80
gcc cag gca atg gat gcg ttg aat ggt acg cgt ctg atc gct ttt gtt 288
Ala Gln Ala Met Asp Ala Leu Asn Gly Thr Arg Leu Ile Ala Phe Val
85 90 95
gag ccc agg aac gaa ttg ata ctg atg caa ttc ttg atg gat cgc ggg 336
Glu Pro Arg Asn Glu Leu Ile Leu Met Gln Phe Leu Met Asp Arg Gly
100 105 110
gct gcg gtg ctt att caa ggt gag cat gcg gtg gac agc aag ggg gtc 384
Ala Ala Val Leu Ile Gln Gly Glu His Ala Val Asp Ser Lys Gly Val
115 120 125
tct cgg cac gac ttt ctg agt acc cca tcc agt gcg gga att gga ggg 432

Ser	Arg	His	Asp	Phe	Leu	Ser	Thr	Pro	Ser	Ser	Ala	Gly	Ile	Gly	Gly		
130						135					140						
gcg	cta	gcc	gac	agc	ctg	gca	aaa	ggg	ggc	tcg	ccg	ttc	tct	att	tcc	480	
Ala	Leu	Ala	Asp	Ser	Leu	Ala	Lys	Gly	Gly	Ser	Pro	Phe	Ser	Ile	Ser		
145					150					155					160		
gtc	cga	gcg	ctt	ggc	tcg	gta	act	gct	cag	cca	aga	agt	aat	cag	agt	528	
Val	Arg	Ala	Leu	Gly	Ser	Val	Thr	Ala	Gln	Pro	Arg	Ser	Asn	Gln	Ser		
				165					170					175			
gag	gtg	gcc	acc	cac	tgg	acg	acc	gct	ctg	ggg	acc	tat	tat	gcc	gat	576	
Glu	Val	Ala	Thr	His	Trp	Thr	Thr	Ala	Leu	Gly	Thr	Tyr	Tyr	Ala	Asp		
			180					185					190				
atc	gca	gtg	ggg	cgc	tgg	gag	ccg	cag	cgc	gaa	gtg	gcc	agc	tat	gga	624	
Ile	Ala	Val	Gly	Arg	Trp	Glu	Pro	Gln	Arg	Glu	Val	Ala	Ser	Tyr	Gly		
		195				200						205					
agt	gga	cta	atc	atg	gcg	gaa	cgg	ctt	gat	cgt	gtt	gcc	tca	acc	ttc	672	
Ser	Gly	Leu	Ile	Met	Ala	Glu	Arg	Leu	Asp	Arg	Val	Ala	Ser	Thr	Phe		
	210					215					220						
att	gca	gat	ctc	tga												687	
Ile	Ala	Asp	Leu														
225																	

<210> 14
 <211> 228
 <212> PRT
 <213> Pseudomonas sp.

<400> 14																	
Met	Thr	Thr	Arg	Arg	Asn	Phe	Leu	Ile	Gly	Ala	Ser	Gln	Val	Gly	Ala		
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Leu	Val	Met	Met	Ser	Pro	Lys	Leu	Val	Phe	Arg	Thr	Pro	Leu	Lys	Gln		
		20					25						30				
Lys	Pro	Val	Arg	Ile	Leu	Ser	Thr	Gly	Leu	Ala	Gly	Glu	Gln	Glu	Phe		
	35				40							45					
His	Ser	Met	Leu	Arg	Ala	Arg	Leu	Thr	His	Thr	Gly	Gln	Val	Asp	Ile		
	50				55						60						
Ala	Ser	Val	Pro	Leu	Asp	Ala	Ala	Ile	Trp	Ala	Ser	Pro	Ala	Arg	Leu		
65				70					75					80			
Ala	Gln	Ala	Met	Asp	Ala	Leu	Asn	Gly	Thr	Arg	Leu	Ile	Ala	Phe	Val		
			85					90						95			
Glu	Pro	Arg	Asn	Glu	Leu	Ile	Leu	Met	Gln	Phe	Leu	Met	Asp	Arg	Gly		
			100				105						110				

Ala Ala Val Leu Ile Gln Gly Glu His Ala Val Asp Ser Lys Gly Val
115 120 125

Ser Arg His Asp Phe Leu Ser Thr Pro Ser Ser Ala Gly Ile Gly Gly
130 135 140

Ala Leu Ala Asp Ser Leu Ala Lys Gly Gly Ser Pro Phe Ser Ile Ser
145 150 155 160

Val Arg Ala Leu Gly Ser Val Thr Ala Gln Pro Arg Ser Asn Gln Ser
165 170 175

Glu Val Ala Thr His Trp Thr Thr Ala Leu Gly Thr Tyr Tyr Ala Asp
180 185 190

Ile Ala Val Gly Arg Trp Glu Pro Gln Arg Glu Val Ala Ser Tyr Gly
195 200 205

Ser Gly Leu Ile Met Ala Glu Arg Leu Asp Arg Val Ala Ser Thr Phe
210 215 220

Ile Ala Asp Leu
225

<210> 15
<211> 1554
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(1551)
<223> product = " Flavoprotein UE-Eugenol-Hydroxylase" /
gene = "ehyB"

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Met Glu Ser Thr Val Val Leu Pro Glu Gly Val Thr Pro Glu Gln Phe
1 5 10 15

acc aaa gcc atc agc gag ttc cgt cag gta ttg ggt gag gac agt gtt 96
Thr Lys Ala Ile Ser Glu Phe Arg Gln Val Leu Gly Glu Asp Ser Val
20 25 30

ctt gtc act gct gaa cga gtt gtt ccc tat acg aaa ctc ctc att cct 144
Leu Val Thr Ala Glu Arg Val Val Pro Tyr Thr Lys Leu Leu Ile Pro
35 40 45

aca cag gat gat gcc cag tac acc ccg gcc ggt gcc ttg act cct tct 192
Thr Gln Asp Asp Ala Gln Tyr Thr Pro Ala Gly Ala Leu Thr Pro Ser
50 55 60

tcg gtg gag cag gtc cag aaa gtc atg ggg atc tgc aat aag tac aag 240
Ser Val Glu Gln Val Gln Lys Val Met Gly Ile Cys Asn Lys Tyr Lys
65 70 75 80

atc ccg gta tgg cca atc tct acc ggt cgg aac tgg ggg tat ggg tcc	288
Ile Pro Val Trp Pro Ile Ser Thr Gly Arg Asn Trp Gly Tyr Gly Ser	
85 90 95	
gct tcg cct gca act cct ggg cag atg att ctt gac ctt cgc aag atg	336
Ala Ser Pro Ala Thr Pro Gly Gln Met Ile Leu Asp Leu Arg Lys Met	
100 105 110	
aac aag atc att gag atc gat gtt gag ggg tgt act gcc ctg ctc gag	384
Asn Lys Ile Ile Glu Ile Asp Val Glu Gly Cys Thr Ala Leu Leu Glu	
115 120 125	
ccg ggc gtt acc tac cag cag ctt cac gat tac atc aag gag cac aat	432
Pro Gly Val Thr Tyr Gln Gln Leu His Asp Tyr Ile Lys Glu His Asn	
130 135 140	
ctg ccc ttg atg ctg gat gtg ccg act att ggg cct atg gtt ggc ccg	480
Leu Pro Leu Met Leu Asp Val Pro Thr Ile Gly Pro Met Val Gly Pro	
145 150 155 160	
gtg ggt aac acg ctg gat cga ggc gtt ggt tat acg ccg tac ggc gag	528
Val Gly Asn Thr Leu Asp Arg Gly Val Gly Tyr Thr Pro Tyr Gly Glu	
165 170 175	
cac ttc atg atg cag tgt ggt atg gaa gtc gtc atg gcc gat ggc gaa	576
His Phe Met Met Gln Cys Gly Met Glu Val Val Met Ala Asp Gly Glu	
180 185 190	
atc ctc cgt act ggt atg ggc tcg gtg ccc aaa gcc aag act tgg cag	624
Ile Leu Arg Thr Gly Met Gly Ser Val Pro Lys Ala Lys Thr Trp Gln	
195 200 205	
gca ttc aaa tgg ggc tat ggt cca tat ctg gac ggt atc ttt acc cag	672
Ala Phe Lys Trp Gly Tyr Gly Pro Tyr Leu Asp Gly Ile Phe Thr Gln	
210 215 220	
tcc aac ttt ggt gtt gtg aca aag ctc ggg att tgg ttg atg ccc aag	720
Ser Asn Phe Gly Val Val Thr Lys Leu Gly Ile Trp Leu Met Pro Lys	
225 230 235 240	
ccg cca gtg atc aag tcg ttt atg atc cgt tat ccc aat gaa gct gat	768
Pro Pro Val Ile Lys Ser Phe Met Ile Arg Tyr Pro Asn Glu Ala Asp	
245 250 255	
gtg gtt aag gca att gat gct ttt cgc ccg ctg cgt att act cag ctg	816
Val Val Lys Ala Ile Asp Ala Phe Arg Pro Leu Arg Ile Thr Gln Leu	
260 265 270	
att cct aac gtc gtt ttg ttc atg cac ggc atg tac gaa acg gca atc	864
Ile Pro Asn Val Val Leu Phe Met His Gly Met Tyr Glu Thr Ala Ile	
275 280 285	
tgc cgg acg cgt gct gag gtt act tcg gac cca ggt cct att tct gaa	912
Cys Arg Thr Arg Ala Glu Val Thr Ser Asp Pro Gly Pro Ile Ser Glu	
290 295 300	

gcg gac gcc cgc aaa gca ttc aaa gag cta ggc gtt ggc tac tgg aac	960
Ala Asp Ala Arg Lys Ala Phe Lys Glu Leu Gly Val Gly Tyr Trp Asn	
305 310 315 320	
ggt tac ttc gcg ctt tac ggc aca gaa gag cag ata gcc gtc aat gaa	1008
Val Tyr Phe Ala Leu Tyr Gly Thr Glu Glu Gln Ile Ala Val Asn Glu	
325 330 335	
aag atc gtc cgc ggc atc ctc gaa ccg acg ggg ggt gag atc ctc acc	1056
Lys Ile Val Arg Gly Ile Leu Glu Pro Thr Gly Gly Glu Ile Leu Thr	
340 345 350	
gaa gag gag gct gga gat aac att ctt ttc cat cac cat aag cag ctc	1104
Glu Glu Glu Ala Gly Asp Asn Ile Leu Phe His His His Lys Gln Leu	
355 360 365	
atg aac ggc gag atg aca ttg gag gaa atg aat atc tac cag tgg cgc	1152
Met Asn Gly Glu Met Thr Leu Glu Glu Met Asn Ile Tyr Gln Trp Arg	
370 375 380	
gga gca ggt ggc ggt gct tgc tgg ttt gca ccg gtt gct cag gtc aag	1200
Gly Ala Gly Gly Gly Ala Cys Trp Phe Ala Pro Val Ala Gln Val Lys	
385 390 395 400	
ggg cat gag gca gag cag cag gtc aag ctt gct cag aag gtg ctt gca	1248
Gly His Glu Ala Glu Gln Gln Val Lys Leu Ala Gln Lys Val Leu Ala	
405 410 415	
aag cat ggg ttc gat tac acg gcg ggc ttt gcg att ggt tgg cgc gat	1296
Lys His Gly Phe Asp Tyr Thr Ala Gly Phe Ala Ile Gly Trp Arg Asp	
420 425 430	
ctt cac cat gtg atc gat gtg ctg tac gac cgt agc aat gcc gac gag	1344
Leu His His Val Ile Asp Val Leu Tyr Asp Arg Ser Asn Ala Asp Glu	
435 440 445	
aaa aag cgc gct tac gct tgc ttt gat gaa ttg atc gac gtc ttt gcg	1392
Lys Lys Arg Ala Tyr Ala Cys Phe Asp Glu Leu Ile Asp Val Phe Ala	
450 455 460	
gcc gaa ggc ttt gca agt tac agg acc aat att gcc ttt atg gac aaa	1440
Ala Glu Gly Phe Ala Ser Tyr Arg Thr Asn Ile Ala Phe Met Asp Lys	
465 470 475 480	
gtc gcc tct aag ttc ggc gct gag aat aag agg gtc aat cag aag atc	1488
Val Ala Ser Lys Phe Gly Ala Glu Asn Lys Arg Val Asn Gln Lys Ile	
485 490 495	
aag gct gcc ctt gat cca aac ggc atc atc gct ccc ggc aag tcg ggc	1536
Lys Ala Ala Leu Asp Pro Asn Gly Ile Ile Ala Pro Gly Lys Ser Gly	
500 505 510	
att cat ctt ccc aaa taa	1554
Ile His Leu Pro Lys	
515	

<210> 16
<211> 517
<212> PRT
<213> Pseudomonas sp.

<400> 16

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Thr	Lys	Ala	Ile	Ser	Glu	Phe	Arg	Gln	Val	Leu	Gly	Glu	Asp	Ser	Val
			20					25					30		
Leu	Val	Thr	Ala	Glu	Arg	Val	Val	Pro	Tyr	Thr	Lys	Leu	Leu	Ile	Pro
			35				40					45			
Thr	Gln	Asp	Asp	Ala	Gln	Tyr	Thr	Pro	Ala	Gly	Ala	Leu	Thr	Pro	Ser
	50					55					60				
Ser	Val	Glu	Gln	Val	Gln	Lys	Val	Met	Gly	Ile	Cys	Asn	Lys	Tyr	Lys
65					70					75					80
Ile	Pro	Val	Trp	Pro	Ile	Ser	Thr	Gly	Arg	Asn	Trp	Gly	Tyr	Gly	Ser
				85					90					95	
Ala	Ser	Pro	Ala	Thr	Pro	Gly	Gln	Met	Ile	Leu	Asp	Leu	Arg	Lys	Met
			100					105					110		
Asn	Lys	Ile	Ile	Glu	Ile	Asp	Val	Glu	Gly	Cys	Thr	Ala	Leu	Leu	Glu
		115					120					125			
Pro	Gly	Val	Thr	Tyr	Gln	Gln	Leu	His	Asp	Tyr	Ile	Lys	Glu	His	Asn
	130					135					140				
Leu	Pro	Leu	Met	Leu	Asp	Val	Pro	Thr	Ile	Gly	Pro	Met	Val	Gly	Pro
145					150					155					160
Val	Gly	Asn	Thr	Leu	Asp	Arg	Gly	Val	Gly	Tyr	Thr	Pro	Tyr	Gly	Glu
				165					170					175	
His	Phe	Met	Met	Gln	Cys	Gly	Met	Glu	Val	Val	Met	Ala	Asp	Gly	Glu
			180					185					190		
Ile	Leu	Arg	Thr	Gly	Met	Gly	Ser	Val	Pro	Lys	Ala	Lys	Thr	Trp	Gln
		195					200					205			
Ala	Phe	Lys	Trp	Gly	Tyr	Gly	Pro	Tyr	Leu	Asp	Gly	Ile	Phe	Thr	Gln
	210					215					220				
Ser	Asn	Phe	Gly	Val	Val	Thr	Lys	Leu	Gly	Ile	Trp	Leu	Met	Pro	Lys
225					230					235					240
Pro	Pro	Val	Ile	Lys	Ser	Phe	Met	Ile	Arg	Tyr	Pro	Asn	Glu	Ala	Asp
				245					250					255	
Val	Val	Lys	Ala	Ile	Asp	Ala	Phe	Arg	Pro	Leu	Arg	Ile	Thr	Gln	Leu

260					265					270					
Ile	Pro	Asn	Val	Val	Leu	Phe	Met	His	Gly	Met	Tyr	Glu	Thr	Ala	Ile
		275					280					285			
Cys	Arg	Thr	Arg	Ala	Glu	Val	Thr	Ser	Asp	Pro	Gly	Pro	Ile	Ser	Glu
		290					295				300				
Ala	Asp	Ala	Arg	Lys	Ala	Phe	Lys	Glu	Leu	Gly	Val	Gly	Tyr	Trp	Asn
305					310					315					320
Val	Tyr	Phe	Ala	Leu	Tyr	Gly	Thr	Glu	Glu	Gln	Ile	Ala	Val	Asn	Glu
				325					330					335	
Lys	Ile	Val	Arg	Gly	Ile	Leu	Glu	Pro	Thr	Gly	Gly	Glu	Ile	Leu	Thr
			340					345					350		
Glu	Glu	Glu	Ala	Gly	Asp	Asn	Ile	Leu	Phe	His	His	His	Lys	Gln	Leu
		355					360					365			
Met	Asn	Gly	Glu	Met	Thr	Leu	Glu	Glu	Met	Asn	Ile	Tyr	Gln	Trp	Arg
	370					375					380				
Gly	Ala	Gly	Gly	Gly	Ala	Cys	Trp	Phe	Ala	Pro	Val	Ala	Gln	Val	Lys
385					390					395					400
Gly	His	Glu	Ala	Glu	Gln	Gln	Val	Lys	Leu	Ala	Gln	Lys	Val	Leu	Ala
				405					410					415	
Lys	His	Gly	Phe	Asp	Tyr	Thr	Ala	Gly	Phe	Ala	Ile	Gly	Trp	Arg	Asp
			420					425					430		
Leu	His	His	Val	Ile	Asp	Val	Leu	Tyr	Asp	Arg	Ser	Asn	Ala	Asp	Glu
		435					440					445			
Lys	Lys	Arg	Ala	Tyr	Ala	Cys	Phe	Asp	Glu	Leu	Ile	Asp	Val	Phe	Ala
	450					455					460				
Ala	Glu	Gly	Phe	Ala	Ser	Tyr	Arg	Thr	Asn	Ile	Ala	Phe	Met	Asp	Lys
465					470					475					480
Val	Ala	Ser	Lys	Phe	Gly	Ala	Glu	Asn	Lys	Arg	Val	Asn	Gln	Lys	Ile
				485					490					495	
Lys	Ala	Ala	Leu	Asp	Pro	Asn	Gly	Ile	Ile	Ala	Pro	Gly	Lys	Ser	Gly
			500					505					510		
Ile	His	Leu	Pro	Lys											
		515													

<210> 17

<211> 861

<212> DNA

<213> Pseudomonas sp.

<220>

<221> CDS

<222> (1)..(858)

<223> gene = "ORF2"

<400> 17

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gag cga cta ggg gac tgc ggt ctt atc ggt caa gtt cga ttg acg gct	96
Glu Arg Leu Gly Asp Cys Gly Leu Ile Gly Gln Val Arg Leu Thr Ala	
20 25 30	
cgc gat cct aaa agg ctt cgt gcc gct gcc gag gaa ggg ttt cag gtc	144
Arg Asp Pro Lys Arg Leu Arg Ala Ala Ala Glu Glu Gly Phe Gln Val	
35 40 45	
gct aag gcg gat tac gcc gat att ggg agt ctt gac cag gca tta cag	192
Ala Lys Ala Asp Tyr Ala Asp Ile Gly Ser Leu Asp Gln Ala Leu Gln	
50 55 60	
ggg gta gac gta tta ctc ctg att tct ggt act gca ccc aat gaa ata	240
Gly Val Asp Val Leu Leu Leu Ile Ser Gly Thr Ala Pro Asn Glu Ile	
65 70 75 80	
agg atc caa cag cat aag tcg gtc atc gac gcg gca aaa cga aac ggc	288
Arg Ile Gln Gln His Lys Ser Val Ile Asp Ala Ala Lys Arg Asn Gly	
85 90 95	
gtg tcg cgt att gtg tat acc agc ttc ata aat cca agt act cgc agc	336
Val Ser Arg Ile Val Tyr Thr Ser Phe Ile Asn Pro Ser Thr Arg Ser	
100 105 110	
agg tct att tgg gcc tcc att cat cgt gaa act gag act tac ctc agg	384
Arg Ser Ile Trp Ala Ser Ile His Arg Glu Thr Glu Thr Tyr Leu Arg	
115 120 125	
cag tct ggg gtg aag ttt acg att gtc cga aat aat cag tat gcg tct	432
Gln Ser Gly Val Lys Phe Thr Ile Val Arg Asn Asn Gln Tyr Ala Ser	
130 135 140	
aac ctg gat ctg ttg ctg ctg agg gct caa gac agc gga ata ttt gcc	480
Asn Leu Asp Leu Leu Leu Leu Arg Ala Gln Asp Ser Gly Ile Phe Ala	
145 150 155 160	
att ccc ggg gcg aag ggg cgg gtg gcg tac gtc tct cat cgc gac gtt	528
Ile Pro Gly Ala Lys Gly Arg Val Ala Tyr Val Ser His Arg Asp Val	
165 170 175	
gcc gct gcc atc tgt agt gtc ctg acg acc gcc gga cac gat aac agg	576
Ala Ala Ala Ile Cys Ser Val Leu Thr Thr Ala Gly His Asp Asn Arg	
180 185 190	
atc tac cag ctc aca ggc tct gag gct ctc aat ggg ctc gag atc gcg	624
Ile Tyr Gln Leu Thr Gly Ser Glu Ala Leu Asn Gly Leu Glu Ile Ala	
195 200 205	

gag att ctt ggt ggg gtg ctc ggg cgt cca gtg cgc gcg atg gat gcc 672
 Glu Ile Leu Gly Gly Val Leu Gly Arg Pro Val Arg Ala Met Asp Ala
 210 215 220

tcg cct gac gag ttt gct gcc agc ttt cgc gag gct gga ttc cct gag 720
 Ser Pro Asp Glu Phe Ala Ala Ser Phe Arg Glu Ala Gly Phe Pro Glu
 225 230 235 240

ttt atg gtt gaa ggc cta cta agc att tat gcc gct tca ggt gct ggg 768
 Phe Met Val Glu Gly Leu Leu Ser Ile Tyr Ala Ala Ser Gly Ala Gly
 245 250 255

gag tac caa tcc gtc agt cct gat gtt ggg ttg ttg acg gga cga cgt 816
 Glu Tyr Gln Ser Val Ser Pro Asp Val Gly Leu Leu Thr Gly Arg Arg
 260 265 270

gcc gaa tcg atg cga act tac ata cag cgt cta gtt tgg cct tga 861
 Ala Glu Ser Met Arg Thr Tyr Ile Gln Arg Leu Val Trp Pro
 275 280 285

<210> 18
 <211> 286
 <212> PRT
 <213> Pseudomonas sp.

<400> 18
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Glu Arg Leu Gly Asp Cys Gly Leu Ile Gly Gln Val Arg Leu Thr Ala
 20 25 30

Arg Asp Pro Lys Arg Leu Arg Ala Ala Ala Glu Glu Gly Phe Gln Val
 35 40 45

Ala Lys Ala Asp Tyr Ala Asp Ile Gly Ser Leu Asp Gln Ala Leu Gln
 50 55 60

Gly Val Asp Val Leu Leu Leu Ile Ser Gly Thr Ala Pro Asn Glu Ile
 65 70 75 80

Arg Ile Gln Gln His Lys Ser Val Ile Asp Ala Ala Lys Arg Asn Gly
 85 90 95

Val Ser Arg Ile Val Tyr Thr Ser Phe Ile Asn Pro Ser Thr Arg Ser
 100 105 110

Arg Ser Ile Trp Ala Ser Ile His Arg Glu Thr Glu Thr Tyr Leu Arg
 115 120 125

Gln Ser Gly Val Lys Phe Thr Ile Val Arg Asn Asn Gln Tyr Ala Ser
 130 135 140

Asn Leu Asp Leu Leu Leu Leu Arg Ala Gln Asp Ser Gly Ile Phe Ala
 145 150 155 160
 Ile Pro Gly Ala Lys Gly Arg Val Ala Tyr Val Ser His Arg Asp Val
 165 170 175
 Ala Ala Ala Ile Cys Ser Val Leu Thr Thr Ala Gly His Asp Asn Arg
 180 185 190
 Ile Tyr Gln Leu Thr Gly Ser Glu Ala Leu Asn Gly Leu Glu Ile Ala
 195 200 205
 Glu Ile Leu Gly Gly Val Leu Gly Arg Pro Val Arg Ala Met Asp Ala
 210 215 220
 Ser Pro Asp Glu Phe Ala Ala Ser Phe Arg Glu Ala Gly Phe Pro Glu
 225 230 235 240
 Phe Met Val Glu Gly Leu Leu Ser Ile Tyr Ala Ala Ser Gly Ala Gly
 245 250 255
 Glu Tyr Gln Ser Val Ser Pro Asp Val Gly Leu Leu Thr Gly Arg Arg
 260 265 270
 Ala Glu Ser Met Arg Thr Tyr Ile Gln Arg Leu Val Trp Pro
 275 280 285

<210> 19

<211> 1011

<212> DNA

<213> Pseudomonas sp.

<220>

<221> CDS

<222> (1)..(1008)

<223> product = "Alkohol-Dehydrogenase" / gene = "adh"

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1

5

10

15

ctc cag cca act cgg ccc cgc ccg cag ttg aat cat ggc gag gtc ctc 96
 Leu Gln Pro Thr Arg Pro Arg Pro Gln Leu Asn His Gly Glu Val Leu

20

25

30

atc agg gtc cat gca gcc tcg ctc aac ttt cgc gat ttg atg atc ttg 144
 Ile Arg Val His Ala Ala Ser Leu Asn Phe Arg Asp Leu Met Ile Leu

35

40

45

gcc ggt cgc tat ccg ggt caa atg aaa ccc gat gtg atc ccg ctg tcc 192
 Ala Gly Arg Tyr Pro Gly Gln Met Lys Pro Asp Val Ile Pro Leu Ser

50

55

60

gat ggt gct ggc gag att gtg gag gtc ggg cct ggc gta tct tcg gag 240

Asp	Gly	Ala	Gly	Glu	Ile	Val	Glu	Val	Gly	Pro	Gly	Val	Ser	Ser	Glu		
65					70					75					80		
gtg	cag	ggt	cag	cgc	gta	gcc	agc	acc	ttt	ttc	cct	aac	tgg	cgg	gcc	288	
Val	Gln	Gly	Gln	Arg	Val	Ala	Ser	Thr	Phe	Phe	Pro	Asn	Trp	Arg	Ala		
				85					90					95			
gga	aag	att	acc	gag	ccg	gct	att	gag	gtg	tcg	ttg	ggc	ttc	ggt	atg	336	
Gly	Lys	Ile	Thr	Glu	Pro	Ala	Ile	Glu	Val	Ser	Leu	Gly	Phe	Gly	Met		
			100					105					110				
gac	ggg	atg	ctc	gcg	gaa	tac	gtt	gct	ctg	ccc	tat	gag	gca	acg	ata	384	
Asp	Gly	Met	Leu	Ala	Glu	Tyr	Val	Ala	Leu	Pro	Tyr	Glu	Ala	Thr	Ile		
		115					120					125					
ccg	ata	ccg	gag	cac	ctg	tcg	tac	gag	gag	gct	gca	aca	ttg	cct	tgc	432	
Pro	Ile	Pro	Glu	His	Leu	Ser	Tyr	Glu	Glu	Ala	Ala	Thr	Leu	Pro	Cys		
	130					135					140						
gcg	gcg	cta	acc	gct	tgg	aat	gcg	ttg	acc	gaa	gtg	ggg	cgt	gtc	aag	480	
Ala	Ala	Leu	Thr	Ala	Trp	Asn	Ala	Leu	Thr	Glu	Val	Gly	Arg	Val	Lys		
145					150					155					160		
gcc	ggt	gat	acg	gtc	ttg	ttg	ctt	ggc	act	ggc	ggt	gtc	tcg	atg	ttc	528	
Ala	Gly	Asp	Thr	Val	Leu	Leu	Leu	Gly	Thr	Gly	Gly	Val	Ser	Met	Phe		
			165					170						175			
gcg	ttg	cag	ttc	gcc	aag	ctc	ttg	ggg	gcg	acg	gtc	att	cac	acc	tcg	576	
Ala	Leu	Gln	Phe	Ala	Lys	Leu	Leu	Gly	Ala	Thr	Val	Ile	His	Thr	Ser		
			180					185					190				
agc	agt	gaa	caa	aag	ctg	gag	agg	gtg	aaa	gcg	atg	ggg	gct	gat	cat	624	
Ser	Ser	Glu	Gln	Lys	Leu	Glu	Arg	Val	Lys	Ala	Met	Gly	Ala	Asp	His		
		195					200					205					
ctg	atc	aac	tac	cgc	aat	tcg	cca	ggg	tgg	gac	cgt	act	gtc	ctg	gat	672	
Leu	Ile	Asn	Tyr	Arg	Asn	Ser	Pro	Gly	Trp	Asp	Arg	Thr	Val	Leu	Asp		
	210					215					220						
ctc	acc	gcg	ggg	cga	ggg	gtt	gac	ctg	gta	gtc	gag	gta	ggg	ggg	gcg	720	
Leu	Thr	Ala	Gly	Arg	Gly	Val	Asp	Leu	Val	Val	Glu	Val	Gly	Gly	Ala		
225					230					235					240		
ggg	acc	ttg	gag	cgc	tca	ctt	cgt	gcg	gtc	aag	gta	ggc	ggt	att	gtc	768	
Gly	Thr	Leu	Glu	Arg	Ser	Leu	Arg	Ala	Val	Lys	Val	Gly	Gly	Ile	Val		
				245					250					255			
gcc	acg	att	ggg	cta	gtg	gct	ggc	gtt	ggc	ccg	att	gac	cca	ttg	ccg	816	
Ala	Thr	Ile	Gly	Leu	Val	Ala	Gly	Val	Gly	Pro	Ile	Asp	Pro	Leu	Pro		
			260					265					270				
ctt	atc	tcc	agg	gct	att	cag	ctc	tcg	ggc	gtc	tat	gtc	ggt	tcc	cgg	864	
Leu	Ile	Ser	Arg	Ala	Ile	Gln	Leu	Ser	Gly	Val	Tyr	Val	Gly	Ser	Arg		
		275					280					285					
gaa	atg	ttt	ctc	tca	atg	aac	aaa	gcc	att	gca	tca	gcc	gaa	atc	aag	912	
Glu	Met	Phe	Leu	Ser	Met	Asn	Lys	Ala	Ile	Ala	Ser	Ala	Glu	Ile	Lys		

290	295	300	
cca gtg atc gat tgc tgc ttc ccc atc gac gag gtt gga gat gct tat			960
Pro Val Ile Asp Cys Cys Phe Pro Ile Asp Glu Val Gly Asp Ala Tyr			
305	310	315	320
gag tac atg cgt agc ggc aat cac ctt ggc aaa gta gtt atc acg atc			1008
Glu Tyr Met Arg Ser Gly Asn His Leu Gly Lys Val Val Ile Thr Ile			
	325	330	335
taa			1011

<210> 20
 <211> 336
 <212> PRT
 <213> Pseudomonas sp.

<400> 20

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	20	25	30
Ile Arg Val His Ala Ala Ser Leu Asn Phe Arg Asp Leu Met Ile Leu			
	35	40	45
Ala Gly Arg Tyr Pro Gly Gln Met Lys Pro Asp Val Ile Pro Leu Ser			
	50	55	60
Asp Gly Ala Gly Glu Ile Val Glu Val Gly Pro Gly Val Ser Ser Glu			
	65	70	75
Val Gln Gly Gln Arg Val Ala Ser Thr Phe Phe Pro Asn Trp Arg Ala			
	85	90	95
Gly Lys Ile Thr Glu Pro Ala Ile Glu Val Ser Leu Gly Phe Gly Met			
	100	105	110
Asp Gly Met Leu Ala Glu Tyr Val Ala Leu Pro Tyr Glu Ala Thr Ile			
	115	120	125
Pro Ile Pro Glu His Leu Ser Tyr Glu Glu Ala Ala Thr Leu Pro Cys			
	130	135	140
Ala Ala Leu Thr Ala Trp Asn Ala Leu Thr Glu Val Gly Arg Val Lys			
	145	150	155
Ala Gly Asp Thr Val Leu Leu Leu Gly Thr Gly Gly Val Ser Met Phe			
	165	170	175
Ala Leu Gln Phe Ala Lys Leu Leu Gly Ala Thr Val Ile His Thr Ser			
	180	185	190
Ser Ser Glu Gln Lys Leu Glu Arg Val Lys Ala Met Gly Ala Asp His			
	195	200	205

Leu Ile Asn Tyr Arg Asn Ser Pro Gly Trp Asp Arg Thr Val Leu Asp
210 215 220

Leu Thr Ala Gly Arg Gly Val Asp Leu Val Val Glu Val Gly Gly Ala
225 230 235 240

Gly Thr Leu Glu Arg Ser Leu Arg Ala Val Lys Val Gly Gly Ile Val
245 250 255

Ala Thr Ile Gly Leu Val Ala Gly Val Gly Pro Ile Asp Pro Leu Pro
260 265 270

Leu Ile Ser Arg Ala Ile Gln Leu Ser Gly Val Tyr Val Gly Ser Arg
275 280 285

Glu Met Phe Leu Ser Met Asn Lys Ala Ile Ala Ser Ala Glu Ile Lys
290 295 300

Pro Val Ile Asp Cys Cys Phe Pro Ile Asp Glu Val Gly Asp Ala Tyr
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Glu Tyr Met Arg Ser Gly Asn His Leu Gly Lys Val Val Ile Thr Ile
325 330 335

<210> 21

<211> 1518

<212> DNA

<213> Pseudomonas sp.

<400> 21

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ccttagccgg aatggcagct tgatggttgc cacgggacca gactggatgt cttgagtgtc 180
gagaattacc agatcgctgc gattttcatc gaggcgacca accacggtca gcaagtaccc 240
gtcaccttcg gcggcggtcg gacttctagg gacgaaggcc ggctcctggg ccgccgaggc 300
ttcgccggag taccagaggt cgtagtcacc tcggtggttg tcccagatgc cgagtgaagt 360
gtacgcgaat atcttctcgg cctgctgatg cgcaagtggg ttgctgggat cgtccacccc 420
cataaagcca tagcgggttgc attgcagggc gaacgaagaa tccatgattg gcatttccgc 480
aaagaaatcg tgtagccggg ttcgcttgat ctctctcgtg ctgctatcga ggtcaatttc 540
ccaacgagtc aggcgtggta cggctttctc aggggcgaag gggttggttt gtgagttggg 600
gaaggggaac ggcaggattt cactttccat aaggtcgata taaatcttgg ttccgacttc 660

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ccaagcattc acaacatgaa atacccagag cgccggtgcc ttgagccagc gaatcagact 720
gccctggcgc ggcgcgagta cgccaatgta gctgcccgagt tccgggtccc acatataaat 780
tggtctgtttc gccttgaggc gggacaggct gttggtggcc ggcataattg ggaaaatgga 840
ccaatttcgg gtaatggcaa agtcgtgcat gaatgcgcca tagggctgct caaaccaagt 900
ttcatgtgtc accttgccgt gcttgctcgac aatgtaatag gccatgtctg gagttgcttc 960
gcccttagct gccgaaccga agaacaacaa gtcacccggt tccgggtcat attttggatg 1020
ggcgggtgtgg gtttggtgg taacttgccc gtcgtagtcg aagtgtccgc gagtttcaag 1080
tgtacgagga tccagttcgt acggtaggcc gtcttccttc accgccagca ccttgccgtg 1140
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tggcgtatta cggtagaacg ttccatttat tgattttggg atttcgccgt caacctctag 1440
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<210> 22

<211> 505

<212> PRT

<213> *Pseudomonas* sp.

<400> 22

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Met Ala Arg Phe Asn Arg Asn Asp Pro Gln Leu Val Gly Thr Leu Leu
 1             5             10             15

Pro Thr Arg Ile Glu Ala Asp Leu Phe Asp Leu Glu Val Asp Gly Glu
      20             25             30

Ile Pro Lys Ser Ile Asn Gly Thr Phe Tyr Arg Asn Thr Pro Glu Pro
      35             40             45

Gln Val Thr Pro Gln Lys Phe His Thr Phe Ile Asp Gly Asp Gly Met
      50             55             60

Ala Ser Ala Phe His Phe Glu Asp Gly His Val Asp Phe Ile Ser Arg
      65             70             75             80

Trp Val Lys Thr Ala Arg Phe Thr Ala Glu Arg Leu Ala Arg Lys Ser
      85             90             95

Leu Phe Gly Met Tyr Arg Asn Pro Tyr Thr Asp Asp Thr Ser Val Lys
      100            105            110

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Gly	Leu	Asp	Arg	Thr	Val	Ala	Asn	Thr	Ser	Ile	Ile	Ser	His	His	Gly	115	120	125	
Lys	Val	Leu	Ala	Val	Lys	Glu	Asp	Gly	Leu	Pro	Tyr	Glu	Leu	Asp	Pro	130	135	140	
Arg	Thr	Leu	Glu	Thr	Arg	Gly	His	Phe	Asp	Tyr	Asp	Gly	Gln	Val	Thr	145	150	155	160
Ser	Gln	Thr	His	Thr	Ala	His	Pro	Lys	Tyr	Asp	Pro	Glu	Thr	Gly	Asp	165	170	175	
Leu	Leu	Phe	Phe	Gly	Ser	Ala	Ala	Lys	Gly	Glu	Ala	Thr	Pro	Asp	Met	180	185	190	
Ala	Tyr	Tyr	Ile	Val	Asp	Lys	His	Gly	Lys	Val	Thr	His	Glu	Thr	Trp	195	200	205	
Phe	Glu	Gln	Pro	Tyr	Gly	Ala	Phe	Met	His	Asp	Phe	Ala	Ile	Thr	Arg	210	215	220	
Asn	Trp	Ser	Ile	Phe	Pro	Ile	Met	Pro	Ala	Thr	Asn	Ser	Leu	Ser	Arg	225	230	235	240
Leu	Lys	Ala	Lys	Gln	Pro	Ile	Tyr	Met	Trp	Glu	Pro	Glu	Leu	Gly	Ser	245	250	255	
Tyr	Ile	Gly	Val	Leu	Ala	Pro	Arg	Gln	Gly	Ser	Leu	Ile	Arg	Trp	Leu	260	265	270	
Lys	Ala	Pro	Ala	Leu	Trp	Val	Phe	His	Val	Val	Asn	Ala	Trp	Glu	Val	275	280	285	
Gly	Thr	Lys	Ile	Tyr	Ile	Asp	Leu	Met	Glu	Ser	Glu	Ile	Leu	Pro	Phe	290	295	300	
Pro	Phe	Pro	Asn	Ser	Gln	Asn	Gln	Pro	Phe	Ala	Pro	Glu	Lys	Ala	Val	305	310	315	320
Pro	Arg	Leu	Thr	Arg	Trp	Glu	Ile	Asp	Leu	Asp	Ser	Ser	Ser	Asp	Glu	325	330	335	
Ile	Lys	Arg	Thr	Arg	Leu	His	Asp	Phe	Phe	Ala	Glu	Met	Pro	Ile	Met	340	345	350	
Asp	Ser	Ser	Phe	Ala	Leu	Gln	Cys	Asn	Arg	Tyr	Gly	Phe	Met	Gly	Val	355	360	365	
Asp	Asp	Pro	Arg	Lys	Pro	Leu	Ala	His	Gln	Gln	Ala	Glu	Lys	Ile	Phe	370	375	380	
Ala	Tyr	Asn	Ser	Leu	Gly	Ile	Trp	Asp	Asn	His	Arg	Gly	Asp	Tyr	Asp	385	390	395	400
Leu	Trp	Tyr	Ser	Gly	Glu	Ala	Ser	Ala	Ala	Gln	Glu	Pro	Ala	Phe	Val	405	410	415	

Pro Arg Ser Pro Thr Ala Ala Glu Gly Asp Gly Tyr Leu Leu Thr Val
 420 425 430
 Val Gly Arg Leu Asp Glu Asn Arg Ser Asp Leu Val Ile Leu Asp Thr
 435 440 445
 Gln Asp Ile Gln Ser Gly Pro Val Ala Thr Ile Lys Leu Pro Phe Arg
 450 455 460
 Leu Arg Ala Ala Leu His Gly Cys Trp Val Pro Asp Leu Asn Glu Thr
 465 470 475 480
 Pro Thr Phe Gln Pro Phe Arg Ala Pro Val Arg Gly Arg Cys Pro Arg
 485 490 495
 Thr Asn Phe Gln Ser Arg Ser Arg Arg
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<210> 23
 <211> 951
 <212> DNA
 <213> Pseudomonas sp.

<220>
 <221> CDS
 <222> (1)..(948)
 <223> gene = "ORF3"

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 Thr Leu Ala Asp Ser Pro Leu His Trp Ala His Thr Leu Asn Gly Ser
 20 25 30
 atg cgt act cat ttc gaa gtc cag cgt ctt gag cgg ggt aga ggt gcc 144
 Met Arg Thr His Phe Glu Val Gln Arg Leu Glu Arg Gly Arg Gly Ala
 35 40 45
 tcc ctt gcc cga tct aga ttt ggc gcg ggt gag ctg tac agt gcc att 192
 Ser Leu Ala Arg Ser Arg Phe Gly Ala Gly Glu Leu Tyr Ser Ala Ile
 50 55 60
 gca cca agc cag gta ctt cgc cac ttc aac gac cag cga aat gct gat 240
 Ala Pro Ser Gln Val Leu Arg His Phe Asn Asp Gln Arg Asn Ala Asp
 65 70 75 80
 gag gct gag cac agc tat ttg att cag ata cga agt ggc gct ttg ggc 288
 Glu Ala Glu His Ser Tyr Leu Ile Gln Ile Arg Ser Gly Ala Leu Gly
 85 90 95
 gtt gca tcc ggc gga aga aag gtg atc ttg gca aat ggt gat tgc tcc 336
 Val Ala Ser Gly Gly Arg Lys Val Ile Leu Ala Asn Gly Asp Cys Ser

100	105	110	
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caa ggt gtc gta ata cgc ttt ccg gtg agt tgg ctg gga gcg tgg gtg Gln Gly Val Val Ile Arg Phe Pro Val Ser Trp Leu Gly Ala Trp Val 130 135 140			432
tcc aat ccg gag gat ctt atc gcc cga cga gtt gat gct gag gta ggg Ser Asn Pro Glu Asp Leu Ile Ala Arg Arg Val Asp Ala Glu Val Gly 145 150 155 160			480
tgg ggt agg gcg cta agc gca tcg gtt tct aat cta gat cca ttg cgc Trp Gly Arg Ala Leu Ser Ala Ser Val Ser Asn Leu Asp Pro Leu Arg 165 170 175			528
atc gac gat tta ggt agc aat gta aat ggc att gca gag cat gtt gct Ile Asp Asp Leu Gly Ser Asn Val Asn Gly Ile Ala Glu His Val Ala 180 185 190			576
atg tta att tca cta gca agt tct gcg gtt agt tct gaa gat ggg ggt Met Leu Ile Ser Leu Ala Ser Ser Ala Val Ser Ser Glu Asp Gly Gly 195 200 205			624
gtg gct ctt cgg aaa atg agg gaa gtg aag aga gta ctc gag cag agt Val Ala Leu Arg Lys Met Arg Glu Val Lys Arg Val Leu Glu Gln Ser 210 215 220			672
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ctc tgt gcg gcg agt gac tcg ggt gct gtg ctg aag gtg gcc atg tcc Leu Cys Ala Ala Ser Asp Ser Gly Ala Val Leu Lys Val Ala Met Ser 275 280 285			864
tca ggt ttt tcg gat tca agc cat ttc agc aag aaa ttt aag gaa aga Ser Gly Phe Ser Asp Ser Ser His Phe Ser Lys Lys Phe Lys Glu Arg 290 295 300			912
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<210> 24
 <211> 316
 <212> PRT
 <213> Pseudomonas sp.

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 20 25 30
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 35 40 45
 Ser Leu Ala Arg Ser Arg Phe Gly Ala Gly Glu Leu Tyr Ser Ala Ile
 50 55 60
 Ala Pro Ser Gln Val Leu Arg His Phe Asn Asp Gln Arg Asn Ala Asp
 65 70 75 80
 Glu Ala Glu His Ser Tyr Leu Ile Gln Ile Arg Ser Gly Ala Leu Gly
 85 90 95
 Val Ala Ser Gly Gly Arg Lys Val Ile Leu Ala Asn Gly Asp Cys Ser
 100 105 110
 Ile Val Asp Ser Arg Gln Asp Phe Thr Leu Ser Ser Asn Ser Ser Thr
 115 120 125
 Gln Gly Val Val Ile Arg Phe Pro Val Ser Trp Leu Gly Ala Trp Val
 130 135 140
 Ser Asn Pro Glu Asp Leu Ile Ala Arg Arg Val Asp Ala Glu Val Gly
 145 150 155 160
 Trp Gly Arg Ala Leu Ser Ala Ser Val Ser Asn Leu Asp Pro Leu Arg
 165 170 175
 Ile Asp Asp Leu Gly Ser Asn Val Asn Gly Ile Ala Glu His Val Ala
 180 185 190
 Met Leu Ile Ser Leu Ala Ser Ser Ala Val Ser Ser Glu Asp Gly Gly
 195 200 205
 Val Ala Leu Arg Lys Met Arg Glu Val Lys Arg Val Leu Glu Gln Ser
 210 215 220
 Phe Ala Asp Ala Asn Leu Gly Pro Glu Ser Val Ser Ser Gln Leu Gly
 225 230 235 240
 Ile Ser Lys Arg Tyr Leu His Tyr Val Phe Ala Ala Cys Gly Thr Thr
 245 250 255
 Phe Gly Arg Glu Leu Leu Glu Ile Arg Leu Gly Lys Ala Tyr Arg Met
 260 265 270

Leu Cys Ala Ala Ser Asp Ser Gly Ala Val Leu Lys Val Ala Met Ser
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 Ser Gly Phe Ser Asp Ser Ser His Phe Ser Lys Lys Phe Lys Glu Arg
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 Tyr Gly Val Ser Pro Val Ser Leu Val Arg Gln Ala
 305 310 315

<210> 25
 <211> 735
 <212> DNA
 <213> Pseudomonas sp.

<220>
 <221> CDS
 <222> (1)..(732)
 <223> product = "Enoyl-CoA-Hydratase" / gene = "ech"

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 Glu Gln Asp Ala Asp Ala Arg Val Leu Val Leu Thr Gly Ala Gly Glu
 20 25 30

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 Ser Trp Thr Ala Gly Met Asp Leu Lys Glu Tyr Phe Arg Glu Thr Asp
 35 40 45

 gct ggc ccc gaa att ctg caa gag aag att cgt cgc gaa gcg tcg acc 192
 Ala Gly Pro Glu Ile Leu Gln Glu Lys Ile Arg Arg Glu Ala Ser Thr
 50 55 60

 tgg cag tgg aag ctc ctg cgg atg tac acc aag ccg acc atc gcg atg 240
 Trp Gln Trp Lys Leu Leu Arg Met Tyr Thr Lys Pro Thr Ile Ala Met
 65 70 75 80

 gtc aat ggc tgg tgc ttc ggc ggc ggc ttc agc ccg ctg gtg gcc tgt 288
 Val Asn Gly Trp Cys Phe Gly Gly Gly Phe Ser Pro Leu Val Ala Cys
 85 90 95

 gat ctg gcc atc tgt gcc gac gag gcc acc ttt ggc ctg tcc gag atc 336
 Asp Leu Ala Ile Cys Ala Asp Glu Ala Thr Phe Gly Leu Ser Glu Ile
 100 105 110

 aac tgg ggc atc ccg ccg ggc aac ctg gtg agt aag gct atg gcc gac 384
 Asn Trp Gly Ile Pro Pro Gly Asn Leu Val Ser Lys Ala Met Ala Asp
 115 120 125

 acc gtg ggt cac cgc gag tcc ctt tac tac atc atg act ggc aag aca 432

Thr	Val	Gly	His	Arg	Glu	Ser	Leu	Tyr	Tyr	Ile	Met	Thr	Gly	Lys	Thr		
130						135					140						
ttt	ggc	ggt	cag	cag	gcc	gcc	aag	atg	ggg	ctt	gtg	aac	cag	agt	gtt	480	
Phe	Gly	Gly	Gln	Gln	Ala	Ala	Lys	Met	Gly	Leu	Val	Asn	Gln	Ser	Val		
145					150					155					160		
ccg	ctg	gcc	gag	ctg	cgc	agt	gtc	act	gta	gag	ctg	gct	cag	aac	ctg	528	
Pro	Leu	Ala	Glu	Leu	Arg	Ser	Val	Thr	Val	Glu	Leu	Ala	Gln	Asn	Leu		
				165					170					175			
ctg	gac	aag	aac	ccc	gta	gtg	ctg	cgt	gcc	gcc	aaa	ata	ggc	ttc	aag	576	
Leu	Asp	Lys	Asn	Pro	Val	Val	Leu	Arg	Ala	Ala	Lys	Ile	Gly	Phe	Lys		
			180					185					190				
cgt	tgc	cgc	gag	ctg	act	tgg	gag	cag	aac	gag	gac	tac	ctg	tac	gcc	624	
Arg	Cys	Arg	Glu	Leu	Thr	Trp	Glu	Gln	Asn	Glu	Asp	Tyr	Leu	Tyr	Ala		
		195					200					205					
aag	ctc	gac	caa	tcc	cgt	ttg	ctc	gat	ccg	gaa	ggc	ggt	cgc	gag	cag	672	
Lys	Leu	Asp	Gln	Ser	Arg	Leu	Leu	Asp	Pro	Glu	Gly	Gly	Arg	Glu	Gln		
	210					215					220						
ggc	atg	aag	cag	ttc	ctt	gac	gag	aaa	agc	atc	aag	ccg	ggc	ttg	cag	720	
Gly	Met	Lys	Gln	Phe	Leu	Asp	Glu	Lys	Ser	Ile	Lys	Pro	Gly	Leu	Gln		
225					230					235					240		
acc	tac	aag	cgc	tga												735	
Thr	Tyr	Lys	Arg														

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 <211> 244
 <212> PRT
 <213> Pseudomonas sp.

<400> 26																	
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Glu	Gln	Asp	Ala	Asp	Ala	Arg	Val	Leu	Val	Leu	Thr	Gly	Ala	Gly	Glu		
			20					25					30				
Ser	Trp	Thr	Ala	Gly	Met	Asp	Leu	Lys	Glu	Tyr	Phe	Arg	Glu	Thr	Asp		
		35					40					45					
Ala	Gly	Pro	Glu	Ile	Leu	Gln	Glu	Lys	Ile	Arg	Arg	Glu	Ala	Ser	Thr		
		50				55					60						
Trp	Gln	Trp	Lys	Leu	Leu	Arg	Met	Tyr	Thr	Lys	Pro	Thr	Ile	Ala	Met		
65					70					75					80		
Val	Asn	Gly	Trp	Cys	Phe	Gly	Gly	Gly	Phe	Ser	Pro	Leu	Val	Ala	Cys		
				85					90						95		

Asp Leu Ala Ile Cys Ala Asp Glu Ala Thr Phe Gly Leu Ser Glu Ile
100 105 110

Asn Trp Gly Ile Pro Pro Gly Asn Leu Val Ser Lys Ala Met Ala Asp
115 120 125

Thr Val Gly His Arg Glu Ser Leu Tyr Tyr Ile Met Thr Gly Lys Thr
130 135 140

Phe Gly Gly Gln Gln Ala Ala Lys Met Gly Leu Val Asn Gln Ser Val
145 150 155 160

Pro Leu Ala Glu Leu Arg Ser Val Thr Val Glu Leu Ala Gln Asn Leu
165 170 175

Leu Asp Lys Asn Pro Val Val Leu Arg Ala Ala Lys Ile Gly Phe Lys
180 185 190

Arg Cys Arg Glu Leu Thr Trp Glu Gln Asn Glu Asp Tyr Leu Tyr Ala
195 200 205

Lys Leu Asp Gln Ser Arg Leu Leu Asp Pro Glu Gly Gly Arg Glu Gln
210 215 220

Gly Met Lys Gln Phe Leu Asp Glu Lys Ser Ile Lys Pro Gly Leu Gln
225 230 235 240

Thr Tyr Lys Arg

<210> 27
<211> 1446
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(1443)
<223> product = Vanillin-Dehydrogenase" / gene = "vdh"

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gat gag cgc acc ttc gag cgt cgt agc ccg ctg acc gga gaa gtg gta 96
Asp Glu Arg Thr Phe Glu Arg Arg Ser Pro Leu Thr Gly Glu Val Val
20 25 30

tcg cgc gtc gct gct gcc agt ttg gaa gat gcg gac gcc gca gtg gcc 144
Ser Arg Val Ala Ala Ala Ser Leu Glu Asp Ala Asp Ala Ala Val Ala
35 40 45

gct gca cag gct gcg ttt cct gaa tgg gcg gcg ctt gct ccg agc gaa	192
Ala Ala Gln Ala Ala Phe Pro Glu Trp Ala Ala Leu Ala Pro Ser Glu	
50 55 60	
cgc cgt gcc cga ctg ctg cga gcg gcg gat ctt cta gag gac cgt tct	240
Arg Arg Ala Arg Leu Leu Arg Ala Ala Asp Leu Leu Glu Asp Arg Ser	
65 70 75 80	
tcc gag ttc acc gcc gca gcg agt gaa act ggc gca gcg gga aac tgg	288
Ser Glu Phe Thr Ala Ala Ala Ser Glu Thr Gly Ala Ala Gly Asn Trp	
85 90 95	
tat ggg ttt aac gtt tac ctg gcg gcg ggc atg ttg cgg gaa gcc gcg	336
Tyr Gly Phe Asn Val Tyr Leu Ala Ala Gly Met Leu Arg Glu Ala Ala	
100 105 110	
gcc atg acc aca cag att cag ggc gat gtc att ccg tcc aat gtg ccc	384
Ala Met Thr Thr Gln Ile Gln Gly Asp Val Ile Pro Ser Asn Val Pro	
115 120 125	
ggc agc ttt gcc atg gcg gtt cga cag cca tgt ggc gtg gtg ctc ggt	432
Gly Ser Phe Ala Met Ala Val Arg Gln Pro Cys Gly Val Val Leu Gly	
130 135 140	
att gcg cct tgg aat gct ccg gta atc ctt ggc gta cgg gct gtt gcg	480
Ile Ala Pro Trp Asn Ala Pro Val Ile Leu Gly Val Arg Ala Val Ala	
145 150 155 160	
atg ccg ttg gca tgc ggc aat acc gtg gtg ttg aaa agc tct gag ctg	528
Met Pro Leu Ala Cys Gly Asn Thr Val Val Leu Lys Ser Ser Glu Leu	
165 170 175	
agt ccc ttt acc cat cgc ctg att ggt cag gtg ttg cat gat gct ggt	576
Ser Pro Phe Thr His Arg Leu Ile Gly Gln Val Leu His Asp Ala Gly	
180 185 190	
ctg ggg gat ggc gtg gtg aat gtc atc agc aat gcc ccg caa gac gct	624
Leu Gly Asp Gly Val Val Asn Val Ile Ser Asn Ala Pro Gln Asp Ala	
195 200 205	
cct gcg gtg gtg gag cga ctg att gca aat cct gcg gta cgt cga gtg	672
Pro Ala Val Val Glu Arg Leu Ile Ala Asn Pro Ala Val Arg Arg Val	
210 215 220	
aac ttc acc ggt tcg acc cac gtt gga cgg atc att ggt gag ctg tct	720
Asn Phe Thr Gly Ser Thr His Val Gly Arg Ile Ile Gly Glu Leu Ser	
225 230 235 240	
gcg cgt cat ctg aag cct gct gtg ctg gaa tta ggt ggt aag gct ccg	768
Ala Arg His Leu Lys Pro Ala Val Leu Glu Leu Gly Gly Lys Ala Pro	
245 250 255	
ttc ttg gtc ttg gac gat gcc gac ctc gat gcg gcg gtc gaa gcg gcg	816
Phe Leu Val Leu Asp Asp Ala Asp Leu Asp Ala Ala Val Glu Ala Ala	
260 265 270	

gcc ttt ggt gcc tac ttc aat cag ggt caa atc tgc atg tcc act gag	864
Ala Phe Gly Ala Tyr Phe Asn Gln Gly Gln Ile Cys Met Ser Thr Glu	
275 280 285	
cg t ctg att gtg aca gca gtc gca gac gcc ttt gtt gaa aag ctg gcg	912
Arg Leu Ile Val Thr Ala Val Ala Asp Ala Phe Val Glu Lys Leu Ala	
290 295 300	
agg aag gtc gcc aca ctg cgt gct ggc gat cct aat gat ccg caa tcg	960
Arg Lys Val Ala Thr Leu Arg Ala Gly Asp Pro Asn Asp Pro Gln Ser	
305 310 315 320	
gtc ttg ggt tcg ttg att gat gcc aat gca ggt caa cgc atc cag gtt	1008
Val Leu Gly Ser Leu Ile Asp Ala Asn Ala Gly Gln Arg Ile Gln Val	
325 330 335	
ctg gtc gat gat gcg ctc gca aaa ggc gcg cgg cag gtc gtc ggt ggt	1056
Leu Val Asp Asp Ala Leu Ala Lys Gly Ala Arg Gln Val Val Gly Gly	
340 345 350	
ggc tta gat ggc agc atc atg cag ccg atg ctg ctt gat cag gtc act	1104
Gly Leu Asp Gly Ser Ile Met Gln Pro Met Leu Leu Asp Gln Val Thr	
355 360 365	
gaa gag atg cgg ctc tac cgt gag gag tcc ttt ggc cct gtt gcc gtt	1152
Glu Glu Met Arg Leu Tyr Arg Glu Glu Ser Phe Gly Pro Val Ala Val	
370 375 380	
gtc ttg cgc ggc gat ggt gat gaa gaa ctg ctg cgt ctt gcc aac gat	1200
Val Leu Arg Gly Asp Gly Asp Glu Glu Leu Leu Arg Leu Ala Asn Asp	
385 390 395 400	
tcg gag ttt ggt ctt tcg gcc gcc att ttc agc cgt gac gtc tcg cgc	1248
Ser Glu Phe Gly Leu Ser Ala Ala Ile Phe Ser Arg Asp Val Ser Arg	
405 410 415	
gca atg gaa ttg gcc cag cgc gtc gat tcg ggc att tgc cat atc aat	1296
Ala Met Glu Leu Ala Gln Arg Val Asp Ser Gly Ile Cys His Ile Asn	
420 425 430	
gga ccg act gtg cat gac gag gct cag atg cca ttc ggt ggg gtg aag	1344
Gly Pro Thr Val His Asp Glu Ala Gln Met Pro Phe Gly Gly Val Lys	
435 440 445	
tcc agc ggc tac ggc agc ttc ggc agt cga gca tcg att gag cac ttt	1392
Ser Ser Gly Tyr Gly Ser Phe Gly Ser Arg Ala Ser Ile Glu His Phe	
450 455 460	
acc cag ctg cgc tgg ctg acc att cag aat ggc ccg cgg cac tat cca	1440
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465 470 475 480	
atc taa	1446
Ile	

<210> 28
 <211> 481
 <212> PRT
 <213> Pseudomonas sp.

<400> 28

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Ser Arg Val Ala Ala Ala Ser Leu Glu Asp Ala Asp Ala Ala Val Ala
 35 40 45

Ala Ala Gln Ala Ala Phe Pro Glu Trp Ala Ala Leu Ala Pro Ser Glu
 50 55 60

Arg Arg Ala Arg Leu Leu Arg Ala Ala Asp Leu Leu Glu Asp Arg Ser
 65 70 75 80

Ser Glu Phe Thr Ala Ala Ala Ser Glu Thr Gly Ala Ala Gly Asn Trp
 85 90 95

Tyr Gly Phe Asn Val Tyr Leu Ala Ala Gly Met Leu Arg Glu Ala Ala
 100 105 110

Ala Met Thr Thr Gln Ile Gln Gly Asp Val Ile Pro Ser Asn Val Pro
 115 120 125

Gly Ser Phe Ala Met Ala Val Arg Gln Pro Cys Gly Val Val Leu Gly
 130 135 140

Ile Ala Pro Trp Asn Ala Pro Val Ile Leu Gly Val Arg Ala Val Ala
 145 150 155 160

Met Pro Leu Ala Cys Gly Asn Thr Val Val Leu Lys Ser Ser Glu Leu
 165 170 175

Ser Pro Phe Thr His Arg Leu Ile Gly Gln Val Leu His Asp Ala Gly
 180 185 190

Leu Gly Asp Gly Val Val Asn Val Ile Ser Asn Ala Pro Gln Asp Ala
 195 200 205

Pro Ala Val Val Glu Arg Leu Ile Ala Asn Pro Ala Val Arg Arg Val
 210 215 220

Asn Phe Thr Gly Ser Thr His Val Gly Arg Ile Ile Gly Glu Leu Ser
 225 230 235 240

Ala Arg His Leu Lys Pro Ala Val Leu Glu Leu Gly Gly Lys Ala Pro
 245 250 255

Phe Leu Val Leu Asp Asp Ala Asp Leu Asp Ala Ala Val Glu Ala Ala
260 265 270
Ala Phe Gly Ala Tyr Phe Asn Gln Gly Gln Ile Cys Met Ser Thr Glu
275 280 285
Arg Leu Ile Val Thr Ala Val Ala Asp Ala Phe Val Glu Lys Leu Ala
290 295 300
Arg Lys Val Ala Thr Leu Arg Ala Gly Asp Pro Asn Asp Pro Gln Ser
305 310 315 320
Val Leu Gly Ser Leu Ile Asp Ala Asn Ala Gly Gln Arg Ile Gln Val
325 330 335
Leu Val Asp Asp Ala Leu Ala Lys Gly Ala Arg Gln Val Val Gly Gly
340 345 350
Gly Leu Asp Gly Ser Ile Met Gln Pro Met Leu Leu Asp Gln Val Thr
355 360 365
Glu Glu Met Arg Leu Tyr Arg Glu Glu Ser Phe Gly Pro Val Ala Val
370 375 380
Val Leu Arg Gly Asp Gly Asp Glu Glu Leu Leu Arg Leu Ala Asn Asp
385 390 395 400
Ser Glu Phe Gly Leu Ser Ala Ala Ile Phe Ser Arg Asp Val Ser Arg
405 410 415
Ala Met Glu Leu Ala Gln Arg Val Asp Ser Gly Ile Cys His Ile Asn
420 425 430
Gly Pro Thr Val His Asp Glu Ala Gln Met Pro Phe Gly Gly Val Lys
435 440 445
Ser Ser Gly Tyr Gly Ser Phe Gly Ser Arg Ala Ser Ile Glu His Phe
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Thr Gln Leu Arg Trp Leu Thr Ile Gln Asn Gly Pro Arg His Tyr Pro
465 470 475 480
Ile

<210> 29

<211> 1770

<212> DNA

<213> Pseudomonas sp.

<220>

<221> CDS

<222> (1)..(1767)

<223> product = "Ferulasaeure-CoA-Synthetase" / gene =

"fcs"

<400> 29

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cgt ctc gag cat tgg gct aag acc cgt cca gaa caa acc tgc gtt gct	96
Arg Leu Glu His Trp Ala Lys Thr Arg Pro Glu Gln Thr Cys Val Ala	
20 25 30	
gcc agg gcg gca aat ggg gaa tgg cgt cgt atc agc tac gcg gaa atg	144
Ala Arg Ala Ala Asn Gly Glu Trp Arg Arg Ile Ser Tyr Ala Glu Met	
35 40 45	
ttc cac aac gtc cgc gcc atc gca cag agc ttg ctt cct tac gga cta	192
Phe His Asn Val Arg Ala Ile Ala Gln Ser Leu Leu Pro Tyr Gly Leu	
50 55 60	
tcg gca gag cgt ccg ctg ctt atc gtc tct gga aat gac ctg gaa cat	240
Ser Ala Glu Arg Pro Leu Leu Ile Val Ser Gly Asn Asp Leu Glu His	
65 70 75 80	
ctt cag ctg gca ttt ggg gct atg tat gcg ggc att ccc tat tgc ccg	288
Leu Gln Leu Ala Phe Gly Ala Met Tyr Ala Gly Ile Pro Tyr Cys Pro	
85 90 95	
gtg tct cct gct tat tca ctg ctg tcg caa gat ttg gcg aag ctg cgt	336
Val Ser Pro Ala Tyr Ser Leu Leu Ser Gln Asp Leu Ala Lys Leu Arg	
100 105 110	
cac atc gta ggt ctt ctg caa ccg gga ctg gtc ttt gct gcc gat gca	384
His Ile Val Gly Leu Leu Gln Pro Gly Leu Val Phe Ala Ala Asp Ala	
115 120 125	
gca cct ttc cag cgc gca att gag acc att ctg ccg gac gac gtg ccc	432
Ala Pro Phe Gln Arg Ala Ile Glu Thr Ile Leu Pro Asp Asp Val Pro	
130 135 140	
gca atc ttc act cga ggc gaa ttg gcc ggg ccg cgc acg gtg agt ttt	480
Ala Ile Phe Thr Arg Gly Glu Leu Ala Gly Arg Arg Thr Val Ser Phe	
145 150 155 160	
gac agc ctg ctg gag cag cct ggt ggg att gag gca gat aat gcc ttt	528
Asp Ser Leu Leu Glu Gln Pro Gly Gly Ile Glu Ala Asp Asn Ala Phe	
165 170 175	
gcg gca act ggc ccc gat acg att gcc aag ttc ttg ttc act tct ggc	576
Ala Ala Thr Gly Pro Asp Thr Ile Ala Lys Phe Leu Phe Thr Ser Gly	
180 185 190	
tct acc aaa ctg cct aag gcg gtg ccg act act cag cga atg ctc tgc	624
Ser Thr Lys Leu Pro Lys Ala Val Pro Thr Thr Gln Arg Met Leu Cys	
195 200 205	

gcc aat cag cag atg ctt ctg caa act ttc ccg gtt ttt ggt gaa gag	672
Ala Asn Gln Gln Met Leu Leu Gln Thr Phe Pro Val Phe Gly Glu Glu	
210 215 220	
ccg ccg gtg ctg gtg gac tgg ttg ccg tgg aac cac acc ttc ggc ggc	720
Pro Pro Val Leu Val Asp Trp Leu Pro Trp Asn His Thr Phe Gly Gly	
225 230 235 240	
agc cac aac atc ggc atc gtg ttg tac aac ggc ggc acg tac tac ctt	768
Ser His Asn Ile Gly Ile Val Leu Tyr Asn Gly Gly Thr Tyr Tyr Leu	
245 250 255	
gac gac ggt aaa cca acc gcc caa ggg ttc gcc gag acg ctt cgc aac	816
Asp Asp Gly Lys Pro Thr Ala Gln Gly Phe Ala Glu Thr Leu Arg Asn	
260 265 270	
ttg agc gaa atc tct ccc act gcg tac ctc act gtg ccg aaa ggc tgg	864
Leu Ser Glu Ile Ser Pro Thr Ala Tyr Leu Thr Val Pro Lys Gly Trp	
275 280 285	
gag gaa tta gtg ggt gcc ctt gag cga gac agt acc ctg cgc gaa cgc	912
Glu Glu Leu Val Gly Ala Leu Glu Arg Asp Ser Thr Leu Arg Glu Arg	
290 295 300	
ttc ttc gct cgc atg aag ctg ttc ttc ttc gcg gcg gct ggg ttg tcg	960
Phe Phe Ala Arg Met Lys Leu Phe Phe Phe Ala Ala Ala Gly Leu Ser	
305 310 315 320	
caa ggg atc tgg gat cgt ttg gac cgg gtc gct gaa cag cac tgt ggt	1008
Gln Gly Ile Trp Asp Arg Leu Asp Arg Val Ala Glu Gln His Cys Gly	
325 330 335	
gag cgc att cgc atg atg gcg ggt ctg ggc atg acg gag act gct cct	1056
Glu Arg Ile Arg Met Met Ala Gly Leu Gly Met Thr Glu Thr Ala Pro	
340 345 350	
tcc tgc act ttt acc acc gga ccg ctg tcg atg gct ggt tac att ggg	1104
Ser Cys Thr Phe Thr Thr Gly Pro Leu Ser Met Ala Gly Tyr Ile Gly	
355 360 365	
ctg cca gcg cct ggc tgc gag gtc aag ctc gtt ccg gtc gat ggg aaa	1152
Leu Pro Ala Pro Gly Cys Glu Val Lys Leu Val Pro Val Asp Gly Lys	
370 375 380	
ttg gaa ggg cgt ttc cat ggt ccg cac gtc atg agc ggc tac tgg cgt	1200
Leu Glu Gly Arg Phe His Gly Pro His Val Met Ser Gly Tyr Trp Arg	
385 390 395 400	
gct cct gaa caa aat gcc caa gcg ttc gac gag gaa ggc tat tac tgc	1248
Ala Pro Glu Gln Asn Ala Gln Ala Phe Asp Glu Glu Gly Tyr Tyr Cys	
405 410 415	
tcc ggt gat gcc atc aaa ttg gca gat cct gcc gat cct cag aaa ggt	1296
Ser Gly Asp Ala Ile Lys Leu Ala Asp Pro Ala Asp Pro Gln Lys Gly	
420 425 430	

ctg atg ttt gac ggt cga att gct gaa gac ttc aag ctg tcc tca ggg 1344
 Leu Met Phe Asp Gly Arg Ile Ala Glu Asp Phe Lys Leu Ser Ser Gly
 435 440 445

gta ttt gtc agc gtt ggg cca ttg cgc acg cgg gcg gtt ctg gaa ggc 1392
 Val Phe Val Ser Val Gly Pro Leu Arg Thr Arg Ala Val Leu Glu Gly
 450 455 460

ggc tct tac gtc ctg gac gta gtg gtt gct gct cct gat cgt gaa tgc 1440
 Gly Ser Tyr Val Leu Asp Val Val Val Ala Ala Pro Asp Arg Glu Cys
 465 470 475 480

ctt gga ttg ctc gtg ttt ccg cgt ctt ctc gac tgc cgt gcc ttg tcg 1488
 Leu Gly Leu Leu Val Phe Pro Arg Leu Leu Asp Cys Arg Ala Leu Ser
 485 490 495

ggg cta gga aaa gag gcg tcg gac gcc gag gtg ctt gcc agt gag ccg 1536
 Gly Leu Gly Lys Glu Ala Ser Asp Ala Glu Val Leu Ala Ser Glu Pro
 500 505 510

gtt cgg gcc tgg ttt gct gac tgg ctc aaa cga ctc aat cga gaa gca 1584
 Val Arg Ala Trp Phe Ala Asp Trp Leu Lys Arg Leu Asn Arg Glu Ala
 515 520 525

act ggc aat gcc agt cgc atc atg tgg gta ggg ctc ctc gat acg ccg 1632
 Thr Gly Asn Ala Ser Arg Ile Met Trp Val Gly Leu Leu Asp Thr Pro
 530 535 540

ccg tcg att gat aag ggc gag gtc act gac aag ggc tcg atc aac cag 1680
 Pro Ser Ile Asp Lys Gly Glu Val Thr Asp Lys Gly Ser Ile Asn Gln
 545 550 555 560

cgc gct gtt ttg caa tgg cgg tcg gcg aaa gtt gat gcg ctg tat cgt 1728
 Arg Ala Val Leu Gln Trp Arg Ser Ala Lys Val Asp Ala Leu Tyr Arg
 565 570 575

ggc gaa gat caa tcc atg ctg cgt gac gag gcc aca ctg tga 1770
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 580 585

<210> 30
 <211> 589
 <212> PRT
 <213> Pseudomonas sp.

<400> 30
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 20 25 30

Ala Arg Ala Ala Asn Gly Glu Trp Arg Arg Ile Ser Tyr Ala Glu Met

35					40					45					
Phe	His	Asn	Val	Arg	Ala	Ile	Ala	Gln	Ser	Leu	Leu	Pro	Tyr	Gly	Leu
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Ser	Ala	Glu	Arg	Pro	Leu	Leu	Ile	Val	Ser	Gly	Asn	Asp	Leu	Glu	His
65					70					75					80
Leu	Gln	Leu	Ala	Phe	Gly	Ala	Met	Tyr	Ala	Gly	Ile	Pro	Tyr	Cys	Pro
				85					90					95	
Val	Ser	Pro	Ala	Tyr	Ser	Leu	Leu	Ser	Gln	Asp	Leu	Ala	Lys	Leu	Arg
			100					105					110		
His	Ile	Val	Gly	Leu	Leu	Gln	Pro	Gly	Leu	Val	Phe	Ala	Ala	Asp	Ala
	115					120						125			
Ala	Pro	Phe	Gln	Arg	Ala	Ile	Glu	Thr	Ile	Leu	Pro	Asp	Asp	Val	Pro
	130					135					140				
Ala	Ile	Phe	Thr	Arg	Gly	Glu	Leu	Ala	Gly	Arg	Arg	Thr	Val	Ser	Phe
145					150					155					160
Asp	Ser	Leu	Leu	Glu	Gln	Pro	Gly	Gly	Ile	Glu	Ala	Asp	Asn	Ala	Phe
				165					170					175	
Ala	Ala	Thr	Gly	Pro	Asp	Thr	Ile	Ala	Lys	Phe	Leu	Phe	Thr	Ser	Gly
			180					185					190		
Ser	Thr	Lys	Leu	Pro	Lys	Ala	Val	Pro	Thr	Thr	Gln	Arg	Met	Leu	Cys
	195					200						205			
Ala	Asn	Gln	Gln	Met	Leu	Leu	Gln	Thr	Phe	Pro	Val	Phe	Gly	Glu	Glu
	210					215					220				
Pro	Pro	Val	Leu	Val	Asp	Trp	Leu	Pro	Trp	Asn	His	Thr	Phe	Gly	Gly
225					230					235					240
Ser	His	Asn	Ile	Gly	Ile	Val	Leu	Tyr	Asn	Gly	Gly	Thr	Tyr	Tyr	Leu
			245						250					255	
Asp	Asp	Gly	Lys	Pro	Thr	Ala	Gln	Gly	Phe	Ala	Glu	Thr	Leu	Arg	Asn
			260					265					270		
Leu	Ser	Glu	Ile	Ser	Pro	Thr	Ala	Tyr	Leu	Thr	Val	Pro	Lys	Gly	Trp
	275						280					285			
Glu	Glu	Leu	Val	Gly	Ala	Leu	Glu	Arg	Asp	Ser	Thr	Leu	Arg	Glu	Arg
	290					295					300				
Phe	Phe	Ala	Arg	Met	Lys	Leu	Phe	Phe	Phe	Ala	Ala	Ala	Gly	Leu	Ser
305					310					315					320
Gln	Gly	Ile	Trp	Asp	Arg	Leu	Asp	Arg	Val	Ala	Glu	Gln	His	Cys	Gly
			325						330					335	
Glu	Arg	Ile	Arg	Met	Met	Ala	Gly	Leu	Gly	Met	Thr	Glu	Thr	Ala	Pro

340										345					350				
Ser	Cys	Thr	Phe	Thr	Thr	Gly	Pro	Leu	Ser	Met	Ala	Gly	Tyr	Ile	Gly				
		355					360					365							
Leu	Pro	Ala	Pro	Gly	Cys	Glu	Val	Lys	Leu	Val	Pro	Val	Asp	Gly	Lys				
	370					375					380								
Leu	Glu	Gly	Arg	Phe	His	Gly	Pro	His	Val	Met	Ser	Gly	Tyr	Trp	Arg				
385					390					395					400				
Ala	Pro	Glu	Gln	Asn	Ala	Gln	Ala	Phe	Asp	Glu	Glu	Gly	Tyr	Tyr	Cys				
				405					410						415				
Ser	Gly	Asp	Ala	Ile	Lys	Leu	Ala	Asp	Pro	Ala	Asp	Pro	Gln	Lys	Gly				
			420					425					430						
Leu	Met	Phe	Asp	Gly	Arg	Ile	Ala	Glu	Asp	Phe	Lys	Leu	Ser	Ser	Gly				
	435						440					445							
Val	Phe	Val	Ser	Val	Gly	Pro	Leu	Arg	Thr	Arg	Ala	Val	Leu	Glu	Gly				
	450					455					460								
Gly	Ser	Tyr	Val	Leu	Asp	Val	Val	Val	Ala	Ala	Pro	Asp	Arg	Glu	Cys				
465					470				475						480				
Leu	Gly	Leu	Leu	Val	Phe	Pro	Arg	Leu	Leu	Asp	Cys	Arg	Ala	Leu	Ser				
				485					490						495				
Gly	Leu	Gly	Lys	Glu	Ala	Ser	Asp	Ala	Glu	Val	Leu	Ala	Ser	Glu	Pro				
			500					505					510						
Val	Arg	Ala	Trp	Phe	Ala	Asp	Trp	Leu	Lys	Arg	Leu	Asn	Arg	Glu	Ala				
	515						520					525							
Thr	Gly	Asn	Ala	Ser	Arg	Ile	Met	Trp	Val	Gly	Leu	Leu	Asp	Thr	Pro				
	530					535					540								
Pro	Ser	Ile	Asp	Lys	Gly	Glu	Val	Thr	Asp	Lys	Gly	Ser	Ile	Asn	Gln				
545					550					555					560				
Arg	Ala	Val	Leu	Gln	Trp	Arg	Ser	Ala	Lys	Val	Asp	Ala	Leu	Tyr	Arg				
				565					570					575					
Gly	Glu	Asp	Gln	Ser	Met	Leu	Arg	Asp	Glu	Ala	Thr	Leu							
			580					585											

<210> 31

<211> 1296

<212> DNA

<213> Pseudomonas sp.

<220>

<221> CDS

<222> (1) .. (1293)

<223> product = "beta-Ketothiolase" / gene = "aat"

<400> 31

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Met Ser Trp Ser Gly Gly Ala Tyr Ser Ala Phe Ser Asp Thr Ala Leu	
1 5 10 15	
gtt gcg gca gtg cgc acc ccc tgg att gat tgc ggg ggt gcc ctg tcg	96
Val Ala Ala Val Arg Thr Pro Trp Ile Asp Cys Gly Gly Ala Leu Ser	
20 25 30	
ctg gtg tcg cct atc gac tta ggg gta aag gtc gct cgc gaa gtt ctg	144
Leu Val Ser Pro Ile Asp Leu Gly Val Lys Val Ala Arg Glu Val Leu	
35 40 45	
atg cgt gcg tcg ctt gaa cca caa atg gtc gat agc gta ctc gca ggc	192
Met Arg Ala Ser Leu Glu Pro Gln Met Val Asp Ser Val Leu Ala Gly	
50 55 60	
tct atg gct caa gca agc ttt gat gct tac ctg ctc ccg cgg cac att	240
Ser Met Ala Gln Ala Ser Phe Asp Ala Tyr Leu Leu Pro Arg His Ile	
65 70 75 80	
ggc ttg tac agc ggt gtt ccc aag tcg gtt ccg gcc ttg ggg gtg cag	288
Gly Leu Tyr Ser Gly Val Pro Lys Ser Val Pro Ala Leu Gly Val Gln	
85 90 95	
cgc att tgc ggc aca ggc ttc gaa ctg ctt cgg cag gcc ggc gag cag	336
Arg Ile Cys Gly Thr Gly Phe Glu Leu Leu Arg Gln Ala Gly Glu Gln	
100 105 110	
att tcc caa ggc gct gat cac gtg ctg tgt gtc gcg gca gag tcc atg	384
Ile Ser Gln Gly Ala Asp His Val Leu Cys Val Ala Ala Glu Ser Met	
115 120 125	
tcg cgt aac ccc atc gcg tcg tat aca cac cgg ggc ggg ttc cgc ctc	432
Ser Arg Asn Pro Ile Ala Ser Tyr Thr His Arg Gly Gly Phe Arg Leu	
130 135 140	
ggt gcg ccc gtt gag ttc aag gat ttt ttg tgg gag gca ttg ttt gat	480
Gly Ala Pro Val Glu Phe Lys Asp Phe Leu Trp Glu Ala Leu Phe Asp	
145 150 155 160	
cct gct cca gga ctc gac atg atc gct acc gca gaa aac ctg gcg cgc	528
Pro Ala Pro Gly Leu Asp Met Ile Ala Thr Ala Glu Asn Leu Ala Arg	
165 170 175	
ctg tac gga atc acc agg gga gaa gct aat tcc tac gcg gta agc agc	576
Leu Tyr Gly Ile Thr Arg Gly Glu Ala Asn Ser Tyr Ala Val Ser Ser	
180 185 190	
ttc gag cgc gca ttg agg gcg caa gag gag aaa tgg att gac caa gag	624
Phe Glu Arg Ala Leu Arg Ala Gln Glu Glu Lys Trp Ile Asp Gln Glu	
195 200 205	
atc gtg gct gtt acg gat gaa cag ttc gat tta gag ggc tac aac agt	672
Ile Val Ala Val Thr Asp Glu Gln Phe Asp Leu Glu Gly Tyr Asn Ser	

210	215	220	
cga gca att gaa ctg cct cgg aag gca aaa ttg ttg atc gtg aca gtc			720
Arg Ala Ile Glu Leu Pro Arg Lys Ala Lys Leu Leu Ile Val Thr Val			
225	230	235	240
atc cgc ggc cta gca gtc ttt gaa gcc ctt tcc cga ttg aag cct gtt			768
Ile Arg Gly Leu Ala Val Phe Glu Ala Leu Ser Arg Leu Lys Pro Val			
	245	250	255
cat tct ggc ggg gtg cag act gcg ggc aac agc tgt gcc gta gtg gac			816
His Ser Gly Gly Val Gln Thr Ala Gly Asn Ser Cys Ala Val Val Asp			
	260	265	270
ggc gcc gcg gcg gct ttg gtg gct cga gag tcg tct gcg aca cag ccg			864
Gly Ala Ala Ala Ala Leu Val Ala Arg Glu Ser Ser Ala Thr Gln Pro			
	275	280	285
gtc ttg gct agg ata ctg gct acc tcc gta gtc ggg atc gag ccc gag			912
Val Leu Ala Arg Ile Leu Ala Thr Ser Val Val Gly Ile Glu Pro Glu			
	290	295	300
cat atg ggg ctc ggc cct gcg ccc gcg att cgc ctg ctg ctt gcg cgt			960
His Met Gly Leu Gly Pro Ala Pro Ala Ile Arg Leu Leu Leu Ala Arg			
305	310	315	320
agt gat ctt agt ttg agg gat atc gac ctc ttt gag ata aac gag gcg			1008
Ser Asp Leu Ser Leu Arg Asp Ile Asp Leu Phe Glu Ile Asn Glu Ala			
	325	330	335
cag gcc gcc caa gtt cta gcg gta cag cat gaa ttg ggt att gag cac			1056
Gln Ala Ala Gln Val Leu Ala Val Gln His Glu Leu Gly Ile Glu His			
	340	345	350
tca aaa ctt aat att tgg ggc ggg gcc att gca ctt gga cac ccg ctt			1104
Ser Lys Leu Asn Ile Trp Gly Gly Ala Ile Ala Leu Gly His Pro Leu			
	355	360	365
gcc gcg acc gga ttg cgt ctc tgc atg acc ctc gct cac caa ttg caa			1152
Ala Ala Thr Gly Leu Arg Leu Cys Met Thr Leu Ala His Gln Leu Gln			
	370	375	380
gct aat aac ttt cga tat gga att gcc tcg gca tgc att ggt ggg gga			1200
Ala Asn Asn Phe Arg Tyr Gly Ile Ala Ser Ala Cys Ile Gly Gly Gly			
385	390	395	400
cag ggg atg gcg gtt ctt tta gag aat ccc cac ttc ggt tcg tcc tct			1248
Gln Gly Met Ala Val Leu Leu Glu Asn Pro His Phe Gly Ser Ser Ser			
	405	410	415
gca cga agt tcg atg att aac aga gtt gac cac tat cca ctg agc taa			1296
Ala Arg Ser Ser Met Ile Asn Arg Val Asp His Tyr Pro Leu Ser			
	420	425	430

<210> 32
 <211> 431
 <212> PRT
 <213> Pseudomonas sp.

<400> 32

Met	Ser	Trp	Ser	Gly	Gly	Ala	Tyr	Ser	Ala	Phe	Ser	Asp	Thr	Ala	Leu
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Val	Ala	Ala	Val	Arg	Thr	Pro	Trp	Ile	Asp	Cys	Gly	Gly	Ala	Leu	Ser
			20					25					30		
Leu	Val	Ser	Pro	Ile	Asp	Leu	Gly	Val	Lys	Val	Ala	Arg	Glu	Val	Leu
		35					40					45			
Met	Arg	Ala	Ser	Leu	Glu	Pro	Gln	Met	Val	Asp	Ser	Val	Leu	Ala	Gly
	50					55					60				
Ser	Met	Ala	Gln	Ala	Ser	Phe	Asp	Ala	Tyr	Leu	Leu	Pro	Arg	His	Ile
	65				70					75					80
Gly	Leu	Tyr	Ser	Gly	Val	Pro	Lys	Ser	Val	Pro	Ala	Leu	Gly	Val	Gln
				85					90					95	
Arg	Ile	Cys	Gly	Thr	Gly	Phe	Glu	Leu	Leu	Arg	Gln	Ala	Gly	Glu	Gln
			100					105					110		
Ile	Ser	Gln	Gly	Ala	Asp	His	Val	Leu	Cys	Val	Ala	Ala	Glu	Ser	Met
		115					120					125			
Ser	Arg	Asn	Pro	Ile	Ala	Ser	Tyr	Thr	His	Arg	Gly	Gly	Phe	Arg	Leu
	130					135					140				
Gly	Ala	Pro	Val	Glu	Phe	Lys	Asp	Phe	Leu	Trp	Glu	Ala	Leu	Phe	Asp
145					150				155					160	
Pro	Ala	Pro	Gly	Leu	Asp	Met	Ile	Ala	Thr	Ala	Glu	Asn	Leu	Ala	Arg
				165					170					175	
Leu	Tyr	Gly	Ile	Thr	Arg	Gly	Glu	Ala	Asn	Ser	Tyr	Ala	Val	Ser	Ser
			180					185					190		
Phe	Glu	Arg	Ala	Leu	Arg	Ala	Gln	Glu	Glu	Lys	Trp	Ile	Asp	Gln	Glu
		195					200					205			
Ile	Val	Ala	Val	Thr	Asp	Glu	Gln	Phe	Asp	Leu	Glu	Gly	Tyr	Asn	Ser
	210					215					220				
Arg	Ala	Ile	Glu	Leu	Pro	Arg	Lys	Ala	Lys	Leu	Leu	Ile	Val	Thr	Val
225					230					235					240
Ile	Arg	Gly	Leu	Ala	Val	Phe	Glu	Ala	Leu	Ser	Arg	Leu	Lys	Pro	Val
				245					250					255	
His	Ser	Gly	Gly	Val	Gln	Thr	Ala	Gly	Asn	Ser	Cys	Ala	Val	Val	Asp
			260					265					270		

Gly Ala Ala Ala Ala Leu Val Ala Arg Glu Ser Ser Ala Thr Gln Pro
 275 280 285
 Val Leu Ala Arg Ile Leu Ala Thr Ser Val Val Gly Ile Glu Pro Glu
 290 295 300
 His Met Gly Leu Gly Pro Ala Pro Ala Ile Arg Leu Leu Leu Ala Arg
 305 310 315 320
 Ser Asp Leu Ser Leu Arg Asp Ile Asp Leu Phe Glu Ile Asn Glu Ala
 325 330 335
 Gln Ala Ala Gln Val Leu Ala Val Gln His Glu Leu Gly Ile Glu His
 340 345 350
 Ser Lys Leu Asn Ile Trp Gly Gly Ala Ile Ala Leu Gly His Pro Leu
 355 360 365
 Ala Ala Thr Gly Leu Arg Leu Cys Met Thr Leu Ala His Gln Leu Gln
 370 375 380
 Ala Asn Asn Phe Arg Tyr Gly Ile Ala Ser Ala Cys Ile Gly Gly Gly
 385 390 395 400
 Gln Gly Met Ala Val Leu Leu Glu Asn Pro His Phe Gly Ser Ser Ser
 405 410 415
 Ala Arg Ser Ser Met Ile Asn Arg Val Asp His Tyr Pro Leu Ser
 420 425 430

<210> 33
 <211> 1596
 <212> DNA
 <213> Pseudomonas sp.
 <220>
 <221> CDS
 <222> (1)..(1593)
 <223> product = "Chemotaxis-Protein" / gene = "mac"

<400> 33
 atg att agt ttc gct cgt atg gca gaa agt tta gga gtc cag gct aaa 48
 Met Ile Ser Phe Ala Arg Met Ala Glu Ser Leu Gly Val Gln Ala Lys
 1 5 10 15
 ctt gcc ctt gcc ttc gca ctc gta tta tgt gtc ggg ctg att gtt acc 96
 Leu Ala Leu Ala Phe Ala Leu Val Leu Cys Val Gly Leu Ile Val Thr
 20 25 30
 ggc acg ggt ttc tac agt gta cat acc ttg tca ggg ttg gtg gaa aag 144
 Gly Thr Gly Phe Tyr Ser Val His Thr Leu Ser Gly Leu Val Glu Lys
 35 40 45
 agc gcg ata gct ggt gag ttg cgg gcg aaa att cag gaa ctg aag gtt 192
 Ser Ala Ile Ala Gly Glu Leu Arg Ala Lys Ile Gln Glu Leu Lys Val

50	55	60	
ctg gag cag cgc gcc tta ttc atc gcc gat gaa ggg tcg ctg aag cag			240
Leu Glu Gln Arg Ala Leu Phe Ile Ala Asp Glu Gly Ser Leu Lys Gln			
65	70	75	80
cgc tcg atc ctc cta agt cag gtg ata gct gaa gtt aat gat gct ata			288
Arg Ser Ile Leu Leu Ser Gln Val Ile Ala Glu Val Asn Asp Ala Ile			
	85	90	95
gat att ttt gac ttt cag cgc gga cga tct gag tta ctt aaa ttc gct			336
Asp Ile Phe Asp Phe Gln Arg Gly Arg Ser Glu Leu Leu Lys Phe Ala			
	100	105	110
gct tct tcg cgc gaa gca agt tac tcc att gag gtc ggt agt aac gct			384
Ala Ser Ser Arg Glu Ala Ser Tyr Ser Ile Glu Val Gly Ser Asn Ala			
	115	120	125
gcg gcc gat aag ttg cag tcg ggc gaa cca agt gac gca ttg atg gtt			432
Ala Ala Asp Lys Leu Gln Ser Gly Glu Pro Ser Asp Ala Leu Met Val			
	130	135	140
gcc gat aaa aag ctg aat gtt gag tat gag caa ttg agt tct gct gtg			480
Ala Asp Lys Lys Leu Asn Val Glu Tyr Glu Gln Leu Ser Ser Ala Val			
	145	150	155
aat gca ctg atg ggg cat tta att gag gat cag aat gaa aaa gtt cca			528
Asn Ala Leu Met Gly His Leu Ile Glu Asp Gln Asn Glu Lys Val Pro			
	165	170	175
cta atc tac tat atg ctt ggc ggc gta act ttg ttt acg atg ctc atg			576
Leu Ile Tyr Tyr Met Leu Gly Gly Val Thr Leu Phe Thr Met Leu Met			
	180	185	190
agt gct tat tcg gtc tgg ttc att tcg cgt cag tta gtt ccg cca tta			624
Ser Ala Tyr Ser Val Trp Phe Ile Ser Arg Gln Leu Val Pro Pro Leu			
	195	200	205
aag tcg acg gtg cag ctt gcc gag cgg att gca tca ggc gac ttg gct			672
Lys Ser Thr Val Gln Leu Ala Glu Arg Ile Ala Ser Gly Asp Leu Ala			
	210	215	220
gat gtc ggg gac agc agg cgc aag gat gaa atc ggt cag ttg caa agt			720
Asp Val Gly Asp Ser Arg Arg Lys Asp Glu Ile Gly Gln Leu Gln Ser			
	225	230	235
gca act agg cgg atg gcg att gga ctg cgt aat ctg gtc ggt gat att			768
Ala Thr Arg Arg Met Ala Ile Gly Leu Arg Asn Leu Val Gly Asp Ile			
	245	250	255
ggt caa agt cgt gcg caa ctg gtt tca tcg tcc agc gac ctt tcg gcc			816
Gly Gln Ser Arg Ala Gln Leu Val Ser Ser Ser Ser Asp Leu Ser Ala			
	260	265	270
atc tgt gct cag gct cag att gat gtc gag tgc cag aag ctt tcg gtc			864

Ile	Cys	Ala	Gln	Ala	Gln	Ile	Asp	Val	Glu	Cys	Gln	Lys	Leu	Ser	Val		
		275					280					285					
gcc	cag	gtc	tct	acc	gcc	gtg	aac	gag	ttg	gtt	gaa	acc	gtc	cag	gca	912	
Ala	Gln	Val	Ser	Thr	Ala	Val	Asn	Glu	Leu	Val	Glu	Thr	Val	Gln	Ala		
		290					295					300					
ata	gca	aaa	agc	acc	gaa	gag	gca	gca	aca	gtc	gcc	gtc	ttg	gcc	gat	960	
Ile	Ala	Lys	Ser	Thr	Glu	Glu	Ala	Ala	Thr	Val	Ala	Val	Leu	Ala	Asp		
305						310					315				320		
gaa	aag	gca	cgc	ggg	ggg	gaa	agt	gtc	gtt	aac	aag	gcc	gtt	gat	ttc	1008	
Glu	Lys	Ala	Arg	Gly	Gly	Glu	Ser	Val	Val	Asn	Lys	Ala	Val	Asp	Phe		
				325						330					335		
att	gag	cac	ctc	tcc	gga	gat	atg	gcg	gaa	ctg	gga	gac	gca	atg	gag	1056	
Ile	Glu	His	Leu	Ser	Gly	Asp	Met	Ala	Glu	Leu	Gly	Asp	Ala	Met	Glu		
			340						345					350			
cgg	ctt	cag	aac	gac	agt	gcg	cag	atc	aat	aag	gta	gta	gac	gtc	att	1104	
Arg	Leu	Gln	Asn	Asp	Ser	Ala	Gln	Ile	Asn	Lys	Val	Val	Asp	Val	Ile		
		355						360					365				
aag	gct	gtg	gcg	gag	cag	acc	aat	ctg	cta	gcc	ctg	aat	gcg	gcg	ata	1152	
Lys	Ala	Val	Ala	Glu	Gln	Thr	Asn	Leu	Leu	Ala	Leu	Asn	Ala	Ala	Ile		
		370					375					380					
gag	gcg	gcc	cgt	gca	gga	gag	cag	ggc	agg	ggc	ttt	gcg	gtc	gtg	gcg	1200	
Glu	Ala	Ala	Arg	Ala	Gly	Glu	Gln	Gly	Arg	Gly	Phe	Ala	Val	Val	Ala		
385						390					395				400		
gat	gag	gtt	cgt	gct	ttg	gcg	atg	cgc	acc	caa	caa	tcg	acc	aaa	gaa	1248	
Asp	Glu	Val	Arg	Ala	Leu	Ala	Met	Arg	Thr	Gln	Gln	Ser	Thr	Lys	Glu		
				405						410					415		
att	gag	agg	cta	gtg	gtt	tca	ttg	cag	cag	gga	agt	gaa	gct	gcg	ggc	1296	
Ile	Glu	Arg	Leu	Val	Val	Ser	Leu	Gln	Gln	Gly	Ser	Glu	Ala	Ala	Gly		
			420						425					430			
gag	ttg	atg	cgg	cgt	ggc	aag	gtc	cgg	acg	cat	gac	gtc	gtt	gga	ttg	1344	
Glu	Leu	Met	Arg	Arg	Gly	Lys	Val	Arg	Thr	His	Asp	Val	Val	Gly	Leu		
		435						440					445				
gcc	cag	caa	gcc	gcg	cgc	cgc	gct	act	cga	aat	tac	cca	gct	gtc	gcc	1392	
Ala	Gln	Gln	Ala	Ala	Arg	Arg	Ala	Thr	Arg	Asn	Tyr	Pro	Ala	Val	Ala		
		450					455				460						
ggc	atc	caa	gcg	atg	aac	tat	cag	atc	gcc	gct	gga	gca	gag	cag	caa	1440	
Gly	Ile	Gln	Ala	Met	Asn	Tyr	Gln	Ile	Ala	Ala	Gly	Ala	Glu	Gln	Gln		
465						470				475					480		
ggg	gct	gct	gtg	gtt	caa	atc	aac	cag	aat	atg	ctt	gaa	gtg	cat	aag	1488	
Gly	Ala	Ala	Val	Val	Gln	Ile	Asn	Gln	Asn	Met	Leu	Glu	Val	His	Lys		
				485						490					495		

atg gct gac gag tcc gcc att aaa gcg gga cag acc atg aag tca tcg	1536
Met Ala Asp Glu Ser Ala Ile Lys Ala Gly Gln Thr Met Lys Ser Ser	
500 505 510	

aag gag ctt gct cac ctc ggc agt gcg cta caa aaa tcc gtt gat cga	1584
Lys Glu Leu Ala His Leu Gly Ser Ala Leu Gln Lys Ser Val Asp Arg	
515 520 525	

ttc cag ctg tag	1596
Phe Gln Leu	
530	

<210> 34

<211> 531

<212> PRT

<213> Pseudomonas sp.

<400> 34

Met Ile Ser Phe Ala Arg Met Ala Glu Ser Leu Gly Val Gln Ala Lys
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Leu Ala Leu Ala Phe Ala Leu Val Leu Cys Val Gly Leu Ile Val Thr
20 25 30

Gly Thr Gly Phe Tyr Ser Val His Thr Leu Ser Gly Leu Val Glu Lys
35 40 45

Ser Ala Ile Ala Gly Glu Leu Arg Ala Lys Ile Gln Glu Leu Lys Val
50 55 60

Leu Glu Gln Arg Ala Leu Phe Ile Ala Asp Glu Gly Ser Leu Lys Gln
65 70 75 80

Arg Ser Ile Leu Leu Ser Gln Val Ile Ala Glu Val Asn Asp Ala Ile
85 90 95

Asp Ile Phe Asp Phe Gln Arg Gly Arg Ser Glu Leu Leu Lys Phe Ala
100 105 110

Ala Ser Ser Arg Glu Ala Ser Tyr Ser Ile Glu Val Gly Ser Asn Ala
115 120 125

Ala Ala Asp Lys Leu Gln Ser Gly Glu Pro Ser Asp Ala Leu Met Val
130 135 140

Ala Asp Lys Lys Leu Asn Val Glu Tyr Glu Gln Leu Ser Ser Ala Val
145 150 155 160

Asn Ala Leu Met Gly His Leu Ile Glu Asp Gln Asn Glu Lys Val Pro
165 170 175

Leu Ile Tyr Tyr Met Leu Gly Gly Val Thr Leu Phe Thr Met Leu Met
180 185 190

Ser Ala Tyr Ser Val Trp Phe Ile Ser Arg Gln Leu Val Pro Pro Leu
195 200 205

Lys Ser Thr Val Gln Leu Ala Glu Arg Ile Ala Ser Gly Asp Leu Ala
 210 215 220

Asp Val Gly Asp Ser Arg Arg Lys Asp Glu Ile Gly Gln Leu Gln Ser
 225 230 235 240

Ala Thr Arg Arg Met Ala Ile Gly Leu Arg Asn Leu Val Gly Asp Ile
 245 250 255

Gly Gln Ser Arg Ala Gln Leu Val Ser Ser Ser Ser Asp Leu Ser Ala
 260 265 270

Ile Cys Ala Gln Ala Gln Ile Asp Val Glu Cys Gln Lys Leu Ser Val
 275 280 285

Ala Gln Val Ser Thr Ala Val Asn Glu Leu Val Glu Thr Val Gln Ala
 290 295 300

Ile Ala Lys Ser Thr Glu Glu Ala Ala Thr Val Ala Val Leu Ala Asp
 305 310 315 320

Glu Lys Ala Arg Gly Gly Glu Ser Val Val Asn Lys Ala Val Asp Phe
 325 330 335

Ile Glu His Leu Ser Gly Asp Met Ala Glu Leu Gly Asp Ala Met Glu
 340 345 350

Arg Leu Gln Asn Asp Ser Ala Gln Ile Asn Lys Val Val Asp Val Ile
 355 360 365

Lys Ala Val Ala Glu Gln Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile
 370 375 380

Glu Ala Ala Arg Ala Gly Glu Gln Gly Arg Gly Phe Ala Val Val Ala
 385 390 395 400

Asp Glu Val Arg Ala Leu Ala Met Arg Thr Gln Gln Ser Thr Lys Glu
 405 410 415

Ile Glu Arg Leu Val Val Ser Leu Gln Gln Gly Ser Glu Ala Ala Gly
 420 425 430

Glu Leu Met Arg Arg Gly Lys Val Arg Thr His Asp Val Val Gly Leu
 435 440 445

Ala Gln Gln Ala Ala Arg Arg Ala Thr Arg Asn Tyr Pro Ala Val Ala
 450 455 460

Gly Ile Gln Ala Met Asn Tyr Gln Ile Ala Ala Gly Ala Glu Gln Gln
 465 470 475 480

Gly Ala Ala Val Val Gln Ile Asn Gln Asn Met Leu Glu Val His Lys
 485 490 495

Met Ala Asp Glu Ser Ala Ile Lys Ala Gly Gln Thr Met Lys Ser Ser
 500 505 510

Lys Glu Leu Ala His Leu Gly Ser Ala Leu Gln Lys Ser Val Asp Arg
515 520 525

Phe Gln Leu
530

<210> 35
<211> 411
<212> DNA
<213> Pseudomonas sp.

<400> 35
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ttcacgttcg tcatcactca gcatcgacgt cgcgtcttgg tcgctctgta ccacgatctt 120
cttcagctct ttgagctgcg tctccccagc tttgctgaga aatatcccat aggaacgctt 180
gtccggcttg cagcgcacgc gcacagcaag gccgagcttc tcgagcttgt tcagcaaggg 240
aaccagttgt ggtggttcga ttgcgagcat ccgcgctagg tcagcctgca taagcccagg 300
gctcgcttcg atgattagaa gtgccgacag ctgcgccggg cgtaggtcat atggcgctcag 360
ggcttcaatc aggccttgag cgagcttcag ctgtgagccg gcgtaaggca t 411

<210> 36
<211> 136
<212> PRT
<213> Pseudomonas sp.

<400> 36
Met Pro Tyr Ala Gly Ser Gln Leu Lys Leu Ala Gln Gly Leu Ile Glu
1 5 10 15
Ala Leu Thr Pro Tyr Asp Leu Arg Pro Ala Gln Leu Ser Ala Leu Leu
20 25 30
Ile Ile Glu Ala Ser Pro Gly Leu Met Gln Ala Asp Leu Ala Arg Met
35 40 45
Leu Ala Ile Glu Pro Pro Gln Leu Val Pro Leu Leu Asn Lys Leu Glu
50 55 60
Lys Leu Gly Leu Ala Val Arg Val Arg Cys Lys Pro Asp Lys Arg Ser
65 70 75 80
Tyr Gly Ile Phe Leu Ser Lys Ala Gly Glu Thr Gln Leu Lys Glu Leu
85 90 95
Lys Lys Ile Val Val Gln Ser Asp Gln Asp Ala Thr Ser Met Leu Ser
100 105 110

Asp Asp Glu Arg Glu Gln Leu Leu Leu Leu Leu His Lys Ile His Ala
 115 120 125

Glu Pro Glu Ala Gln Gln Leu Gly
 130 135

<210> 37

<211> 1446

<212> DNA

<213> Pseudomonas sp.

<220>

<221> CDS

<222> (1)..(1443)

<223> product = "Coniferylaldehyd-Dehydrogenase" / gene
 = "caldh"

<400> 37

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Met Ser Ile Leu Gly Leu Asn Gly Ala Pro Val Gly Ala Glu Gln Leu	
1 5 10 15	
ggc tcg gct ctt gat cgc atg aag aag gcg cac ctg gag cag ggg cct	96
Gly Ser Ala Leu Asp Arg Met Lys Lys Ala His Leu Glu Gln Gly Pro	
20 25 30	
gca aac ttg gag ctg cgt ctg agt agg ctg gat cgt gcg att gca atg	144
Ala Asn Leu Glu Leu Arg Leu Ser Arg Leu Asp Arg Ala Ile Ala Met	
35 40 45	
ctt ctg gaa aat cgt gaa gca att gcc gac gcg gtt tct gct gac ttt	192
Leu Leu Glu Asn Arg Glu Ala Ile Ala Asp Ala Val Ser Ala Asp Phe	
50 55 60	
ggc aat cgc agc cgt gag caa aca ctg ctt tgc gac att gct ggc tcg	240
Gly Asn Arg Ser Arg Glu Gln Thr Leu Leu Cys Asp Ile Ala Gly Ser	
65 70 75 80	
gtg gca agc ctg aag gat agc cgc gag cac gtg gcc aaa tgg atg gag	288
Val Ala Ser Leu Lys Asp Ser Arg Glu His Val Ala Lys Trp Met Glu	
85 90 95	
ccc gaa cat cac aag gcg atg ttt cca ggg gcg gag gca cgc gtt gag	336
Pro Glu His His Lys Ala Met Phe Pro Gly Ala Glu Ala Arg Val Glu	
100 105 110	
ttt cag ccg ctg ggt gtc gtt ggg gtc att agt ccc tgg aac ttc cct	384
Phe Gln Pro Leu Gly Val Val Gly Val Ile Ser Pro Trp Asn Phe Pro	
115 120 125	
atc gta ctg gcc ttt ggg ccg ctg gcc ggc ata ttc gca gca ggt aat	432
Ile Val Leu Ala Phe Gly Pro Leu Ala Gly Ile Phe Ala Ala Gly Asn	
130 135 140	

cgc gcc atg ctc aag ccg tcc gag ctt acc ccg cgg act tct gcc ctg	480
Arg Ala Met Leu Lys Pro Ser Glu Leu Thr Pro Arg Thr Ser Ala Leu	
145 150 155 160	
ctt gcg gag cta att gct cgt tac ttc gat gaa act gag ctg act aca	528
Leu Ala Glu Leu Ile Ala Arg Tyr Phe Asp Glu Thr Glu Leu Thr Thr	
165 170 175	
gtg ctg ggc gac gct gaa gtc ggt gcg ctg ttc agt gct cag cct ttc	576
Val Leu Gly Asp Ala Glu Val Gly Ala Leu Phe Ser Ala Gln Pro Phe	
180 185 190	
gat cat ctg atc ttc acc ggc ggc act gcc gtg gcc aag cac atc atg	624
Asp His Leu Ile Phe Thr Gly Gly Thr Ala Val Ala Lys His Ile Met	
195 200 205	
cgt gcc gcg gcg gat aac cta gtg ccc gtt acc ctg gaa ttg ggt ggc	672
Arg Ala Ala Ala Asp Asn Leu Val Pro Val Thr Leu Glu Leu Gly Gly	
210 215 220	
aaa tcg ccg gtg atc gtt tcc cgc agt gca gat atg gcg gac gtt gca	720
Lys Ser Pro Val Ile Val Ser Arg Ser Ala Asp Met Ala Asp Val Ala	
225 230 235 240	
caa cgg gtg ttg acg gtg aaa acc ttc aat gcc ggg caa atc tgt ctg	768
Gln Arg Val Leu Thr Val Lys Thr Phe Asn Ala Gly Gln Ile Cys Leu	
245 250 255	
gca ccg gac tat gtg ctg ctg ccg gaa gaa tcg ctg gat agc ttt gtc	816
Ala Pro Asp Tyr Val Leu Leu Pro Glu Glu Ser Leu Asp Ser Phe Val	
260 265 270	
gcc gag gcg acg cgc ttc gtg gcc gca atg tat ccc tcg ctt cta gat	864
Ala Glu Ala Thr Arg Phe Val Ala Ala Met Tyr Pro Ser Leu Leu Asp	
275 280 285	
aat ccg gat tac acg tcg atc atc aat gcc cga aat ttc gac cgt ctg	912
Asn Pro Asp Tyr Thr Ser Ile Ile Asn Ala Arg Asn Phe Asp Arg Leu	
290 295 300	
cat cgc tac ctg act gat gcg cag gca aag gga ggg cgc gtc att gaa	960
His Arg Tyr Leu Thr Asp Ala Gln Ala Lys Gly Gly Arg Val Ile Glu	
305 310 315 320	
atc aat cct gcg gcc gaa gag ttg ggg gat agt ggt atc agg aag atc	1008
Ile Asn Pro Ala Ala Glu Glu Leu Gly Asp Ser Gly Ile Arg Lys Ile	
325 330 335	
gcg ccc act ttg atc gtg aat gtg tcg gat gaa atg ctg gtc ttg aac	1056
Ala Pro Thr Leu Ile Val Asn Val Ser Asp Glu Met Leu Val Leu Asn	
340 345 350	
gag gag atc ttt ggt ccg ctg ctc ccg atc aag act tat cgt gat ttc	1104
Glu Glu Ile Phe Gly Pro Leu Leu Pro Ile Lys Thr Tyr Arg Asp Phe	
355 360 365	

gac tcg gct atc gac tac gtc aac agc aag cag cga cca ctt gcc tcg	1152
Asp Ser Ala Ile Asp Tyr Val Asn Ser Lys Gln Arg Pro Leu Ala Ser	
370 375 380	
tac ttc ttc ggc gaa gat gcg gtt gag cgt gag caa gtg ctt aag cgt	1200
Tyr Phe Phe Gly Glu Asp Ala Val Glu Arg Glu Gln Val Leu Lys Arg	
385 390 395 400	
acg gtt tcg ggc gcc gtg gtc gtg aac gat gtc atg agc cat gtg atg	1248
Thr Val Ser Gly Ala Val Val Val Asn Asp Val Met Ser His Val Met	
405 410 415	
atg gat acg ctt cca ttt ggt ggt gtg ggg cac tcg ggg atg ggg gca	1296
Met Asp Thr Leu Pro Phe Gly Gly Val Gly His Ser Gly Met Gly Ala	
420 425 430	
tat cac ggc att tat ggt ttc cga acc ttc agc cat gcc aag cct gtt	1344
Tyr His Gly Ile Tyr Gly Phe Arg Thr Phe Ser His Ala Lys Pro Val	
435 440 445	
ctc gtg caa agt cct gtg ggt gag tcg aac ttg gcg atg cgc gca ccc	1392
Leu Val Gln Ser Pro Val Gly Glu Ser Asn Leu Ala Met Arg Ala Pro	
450 455 460	
tac gga gaa gcg atc cac gga ctg ctc tct gtc ctc ctt tca acg gag	1440
Tyr Gly Glu Ala Ile His Gly Leu Leu Ser Val Leu Leu Ser Thr Glu	
465 470 475 480	
tgt tag	1446
Cys	

<210> 38

<211> 481

<212> PRT

<213> Pseudomonas sp.

<400> 38

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Gly Ser Ala Leu Asp Arg Met Lys Lys Ala His Leu Glu Gln Gly Pro
20 25 30

Ala Asn Leu Glu Leu Arg Leu Ser Arg Leu Asp Arg Ala Ile Ala Met
35 40 45

Leu Leu Glu Asn Arg Glu Ala Ile Ala Asp Ala Val Ser Ala Asp Phe
50 55 60

Gly Asn Arg Ser Arg Glu Gln Thr Leu Leu Cys Asp Ile Ala Gly Ser
65 70 75 80

Val Ala Ser Leu Lys Asp Ser Arg Glu His Val Ala Lys Trp Met Glu
85 90 95

Pro Glu His His Lys Ala Met Phe Pro Gly Ala Glu Ala Arg Val Glu

100					105					110					
Phe	Gln	Pro	Leu	Gly	Val	Val	Gly	Val	Ile	Ser	Pro	Trp	Asn	Phe	Pro
		115					120					125			
Ile	Val	Leu	Ala	Phe	Gly	Pro	Leu	Ala	Gly	Ile	Phe	Ala	Ala	Gly	Asn
	130					135					140				
Arg	Ala	Met	Leu	Lys	Pro	Ser	Glu	Leu	Thr	Pro	Arg	Thr	Ser	Ala	Leu
145						150					155				160
Leu	Ala	Glu	Leu	Ile	Ala	Arg	Tyr	Phe	Asp	Glu	Thr	Glu	Leu	Thr	Thr
				165					170					175	
Val	Leu	Gly	Asp	Ala	Glu	Val	Gly	Ala	Leu	Phe	Ser	Ala	Gln	Pro	Phe
			180					185					190		
Asp	His	Leu	Ile	Phe	Thr	Gly	Gly	Thr	Ala	Val	Ala	Lys	His	Ile	Met
		195					200					205			
Arg	Ala	Ala	Ala	Asp	Asn	Leu	Val	Pro	Val	Thr	Leu	Glu	Leu	Gly	Gly
	210					215					220				
Lys	Ser	Pro	Val	Ile	Val	Ser	Arg	Ser	Ala	Asp	Met	Ala	Asp	Val	Ala
225						230					235				240
Gln	Arg	Val	Leu	Thr	Val	Lys	Thr	Phe	Asn	Ala	Gly	Gln	Ile	Cys	Leu
				245					250					255	
Ala	Pro	Asp	Tyr	Val	Leu	Leu	Pro	Glu	Glu	Ser	Leu	Asp	Ser	Phe	Val
			260					265					270		
Ala	Glu	Ala	Thr	Arg	Phe	Val	Ala	Ala	Met	Tyr	Pro	Ser	Leu	Leu	Asp
		275					280					285			
Asn	Pro	Asp	Tyr	Thr	Ser	Ile	Ile	Asn	Ala	Arg	Asn	Phe	Asp	Arg	Leu
	290					295					300				
His	Arg	Tyr	Leu	Thr	Asp	Ala	Gln	Ala	Lys	Gly	Gly	Arg	Val	Ile	Glu
305						310					315				320
Ile	Asn	Pro	Ala	Ala	Glu	Glu	Leu	Gly	Asp	Ser	Gly	Ile	Arg	Lys	Ile
				325					330					335	
Ala	Pro	Thr	Leu	Ile	Val	Asn	Val	Ser	Asp	Glu	Met	Leu	Val	Leu	Asn
			340					345					350		
Glu	Glu	Ile	Phe	Gly	Pro	Leu	Leu	Pro	Ile	Lys	Thr	Tyr	Arg	Asp	Phe
		355					360					365			
Asp	Ser	Ala	Ile	Asp	Tyr	Val	Asn	Ser	Lys	Gln	Arg	Pro	Leu	Ala	Ser
	370					375					380				
Tyr	Phe	Phe	Gly	Glu	Asp	Ala	Val	Glu	Arg	Glu	Gln	Val	Leu	Lys	Arg
385						390					395				400
Thr	Val	Ser	Gly	Ala	Val	Val	Val	Asn	Asp	Val	Met	Ser	His	Val	Met

	405		410		415
Met Asp Thr	Leu Pro Phe Gly Gly	Val Gly His Ser Gly	Met Gly Ala		
	420	425	430		
Tyr His Gly	Ile Tyr Gly Phe Arg Thr Phe Ser His	Ala Lys Pro Val			
	435	440	445		
Leu Val Gln Ser Pro Val	Gly Glu Ser Asn Leu	Ala Met Arg Ala Pro			
	450	455	460		
Tyr Gly Glu Ala Ile His	Gly Leu Leu Ser Val	Leu Leu Ser Thr Glu			
465	470	475	480		

Cys

<210> 39
 <211> 1827
 <212> DNA
 <213> Pseudomonas sp.

<400> 39
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 gtctccact tcttgcagcg tcatcgcgct caggtccttt gagtcaagcg gcgagtcgat 180
 tgtgctggtc ggtttggaga aggaagtact tgggctgccg gtttcctgtg gctgattatc 240
 ttgagcggtg gccaggatgc cgctggcccc aatggagaac atcggttgag tcagtcgttc 300
 accgctagtg aagaggtggc tcacgtcaat ggctccatcc tccggagcgc tgatgactcc 360
 gcgctccacc aaattttgaa gctcccggat gtttcctgga aagtcgtagc caagcagggc 420
 attggctgca cgtggagtga atccgctgac caccgggcta tgacgctgat tgaagcggtg 480
 caggaaatag gtcatcagga ggggaatgtc ttccttcctc tctcgaagcg gcgggaggtg 540
 gatcgggtaa acattgaggc ggaaaaaaag gtcctcgcgg aactcgccgc gctggacgcc 600
 tgcgcggaaga tcgacattgg ttgcggctac cacacggacg tcaaccttga gtgtcctgct 660
 tccgccaacc cgttcgacct ccgactcttg cagggcgcgga agtaacttcc cttggggccac 720
 gaggcttagc gtccctatct cgtcaaggaa tagtgtgccg cccgaagcgc gctcgaaccg 780
 tcttgctcga gattgggtgg cgccggtaaa cgccccccgt tcgacgccga acaactcgga 840
 ctccatcagg gtttcgggaa tacgtgcgca attgaccgca acaaacgggc cgtcgtgtct 900

Asp Ala Ala Leu Leu Lys Glu Arg Phe Ser Asn Ala Asp Pro Leu Ser
 100 105 110

Leu Phe Ala Ala Gly Pro Asn Leu His Ser Leu Glu Gly Ala Val Arg
 115 120 125

Val Glu Pro Ile His Phe Asp Phe Asp Met Asp Leu Gly Thr Tyr Tyr
 130 135 140

Gly Glu Phe Leu Trp His His Ser Ser Glu Asp Asp Glu His Ile Ala
 145 150 155 160

His Tyr Gly Ile Gly Thr Glu Pro Ala Cys Trp Thr Gln Thr Gly Tyr
 165 170 175

Ala Ile Gly Tyr Thr Ser Ala Leu Val Gly Arg Leu Ile Leu Tyr Arg
 180 185 190

Glu Val Glu Cys Arg Ser Thr Gly Ser Gln Ile Cys Arg Met Ile Gly
 195 200 205

Lys Pro Ala Glu Glu Trp Glu Asp Ala Glu Glu Asp Leu Ala Ala Leu
 210 215 220

Ser Ala Thr Ile Cys Arg Gln Pro Ser Thr Pro Gln Arg Arg Arg Thr
 225 230 235 240

Gln Gln Gly Gln Arg Asn Thr Pro His His Ser Ala Ala Asp Ser Ser
 245 250 255

Thr Ala Ser Glu His Asp Met Val Gly Ile Ser Ser Ala Phe Asn Ala
 260 265 270

Ala Cys His Met Leu Lys Arg Val Ala Pro Thr Glu Ala Thr Val Leu
 275 280 285

Phe Thr Gly Glu Ser Gly Val Gly Lys Glu Met Phe Ala Arg Met Leu
 290 295 300

His Arg Ile Ser Pro Arg His Asp Gly Pro Phe Val Ala Val Asn Cys
 305 310 315 320

Ala Arg Ile Pro Glu Thr Leu Met Glu Ser Glu Leu Phe Gly Val Glu
 325 330 335

Arg Gly Ala Phe Thr Gly Ala Thr Gln Ser Arg Ala Gly Arg Phe Glu
 340 345 350

Arg Ala Ser Gly Gly Thr Leu Phe Leu Asp Glu Ile Gly Thr Leu Ser
 355 360 365

Leu Val Ala Gln Gly Lys Leu Leu Arg Ala Leu Gln Glu Ser Glu Val
 370 375 380

Glu Arg Val Gly Gly Ser Arg Thr Leu Lys Val Asp Val Arg Val Val
 385 390 395 400

Ala Ala Thr Asn Val Asp Leu Arg Ala Gly Val Gln Arg Gly Glu Phe
 405 410 415
 Arg Glu Asp Leu Phe Phe Arg Leu Asn Val Tyr Pro Ile His Leu Pro
 420 425 430
 Pro Leu Arg Glu Arg Lys Glu Asp Ile Pro Leu Leu Met Thr Tyr Phe
 435 440 445
 Leu His Arg Phe Asn Gln Arg His Ser Arg Val Val Ser Gly Phe Thr
 450 455 460
 Pro Arg Ala Ala Asn Ala Leu Leu Gly Tyr Asp Phe Pro Gly Asn Ile
 465 470 475 480
 Arg Glu Leu Gln Asn Leu Val Glu Arg Gly Val Ile Ser Ala Pro Glu
 485 490 495
 Asp Gly Ala Ile Asp Val Ser His Leu Phe Thr Ser Gly Glu Arg Leu
 500 505 510
 Thr Gln Pro Met Phe Ser Ile Gly Ala Ser Gly Ile Leu Ala Thr Ala
 515 520 525
 Gln Asp Asn Gln Pro Gln Glu Thr Gly Ser Pro Ser Thr Ser Phe Ser
 530 535 540
 Lys Pro Thr Ser Thr Ile Asp Ser Pro Leu Asp Ser Lys Asp Leu Ser
 545 550 555 560
 Ala Met Thr Leu Gln Glu Val Glu Asp Ala Met Ile Ser His Ala Leu
 565 570 575
 Gly Gln Val Lys Gly Asn Val Ser Glu Ala Ala Arg Arg Leu Gly Leu
 580 585 590
 Thr Arg Ala Gln Leu Ser Tyr Arg Ile Ser Arg Arg Pro Leu Asp Lys
 595 600 605

<210> 41
 <211> 768
 <212> DNA
 <213> Pseudomonas sp.

 <220>
 <221> CDS
 <222> (1)..(765)
 <223> product = "Coniferylalcohol-Dehydrogenase" / gene
 = "cadh"

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 Met Gln Leu Thr Asn Lys Lys Ile Val Val Thr Gly Val Ser Ser Gly

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atc ggt gcc gaa act gcc cgc gtt ctg cgc tct cac ggc gcc aca gtg	96			
Ile Gly Ala Glu Thr Ala Arg Val Leu Arg Ser His Gly Ala Thr Val				
20 25 30				
att ggc gta gat cgc aac atg ccg agc ctg act ctg gat gct ttc gtt	144			
Ile Gly Val Asp Arg Asn Met Pro Ser Leu Thr Leu Asp Ala Phe Val				
35 40 45				
cag gct gac ctg agc cat cct gaa ggc atc gat aag gcc atc tct cag	192			
Gln Ala Asp Leu Ser His Pro Glu Gly Ile Asp Lys Ala Ile Ser Gln				
50 55 60				
ctg ccg gag aaa att gac gga ctc tgc aat atc gcc ggg gtg ccc ggc	240			
Leu Pro Glu Lys Ile Asp Gly Leu Cys Asn Ile Ala Gly Val Pro Gly				
65 70 75 80				
act gcc gat cct cag ctc gtc gca aac gtg aac tac ctg ggt cta aag	288			
Thr Ala Asp Pro Gln Leu Val Ala Asn Val Asn Tyr Leu Gly Leu Lys				
85 90 95				
tat ctg acc gag gca gtc ctg tcg cgc att caa ccc ggt ggt tcg att	336			
Tyr Leu Thr Glu Ala Val Leu Ser Arg Ile Gln Pro Gly Gly Ser Ile				
100 105 110				
gtc aac gtg tcc tct gtg ctt ggc gcc gag tgg ccg gcc cgc ctt cag	384			
Val Asn Val Ser Ser Val Leu Gly Ala Glu Trp Pro Ala Arg Leu Gln				
115 120 125				
ttg cat aag gag ctg ggg agt gtt gtt gga ttc tcc gaa ggc cag gca	432			
Leu His Lys Glu Leu Gly Ser Val Val Gly Phe Ser Glu Gly Gln Ala				
130 135 140				
tgg ctt aag cag aat cca gtg gcc ccc gaa ttc tgc tac cag tat ttc	480			
Trp Leu Lys Gln Asn Pro Val Ala Pro Glu Phe Cys Tyr Gln Tyr Phe				
145 150 155 160				
aaa gaa gca ctg atc gtt tgg tct caa gtt cag gcg cag gaa tgg ttc	528			
Lys Glu Ala Leu Ile Val Trp Ser Gln Val Gln Ala Gln Glu Trp Phe				
165 170 175				
atg agg acg tct gta cgc atg aac tgc atc gcc ccc ggc cct gta ttc	576			
Met Arg Thr Ser Val Arg Met Asn Cys Ile Ala Pro Gly Pro Val Phe				
180 185 190				
act ccc att ctc aat gag ttc gtc acc atg ctg ggt caa gag cgg act	624			
Thr Pro Ile Leu Asn Glu Phe Val Thr Met Leu Gly Gln Glu Arg Thr				
195 200 205				
cag gcg gac gct cat cgt att aag cgc cca gca tat gcc gat gaa gtg	672			
Gln Ala Asp Ala His Arg Ile Lys Arg Pro Ala Tyr Ala Asp Glu Val				
210 215 220				
gcc gcg gtg att gca ttc atg tgt gct gag gag tca cgt tgg atc aac	720			
Ala Ala Val Ile Ala Phe Met Cys Ala Glu Ser Arg Trp Ile Asn				
225 230 235 240				

ggc ata aat att cca gtg gac gga ggt ttg gca tcg acc tac gtg taa 768
 Gly Ile Asn Ile Pro Val Asp Gly Gly Leu Ala Ser Thr Tyr Val
 245 250 255

<210> 42
 <211> 255
 <212> PRT
 <213> Pseudomonas sp.

<400> 42
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 Ile Gly Val Asp Arg Asn Met Pro Ser Leu Thr Leu Asp Ala Phe Val
 35 40 45
 Gln Ala Asp Leu Ser His Pro Glu Gly Ile Asp Lys Ala Ile Ser Gln
 50 55 60
 Leu Pro Glu Lys Ile Asp Gly Leu Cys Asn Ile Ala Gly Val Pro Gly
 65 70 75 80
 Thr Ala Asp Pro Gln Leu Val Ala Asn Val Asn Tyr Leu Gly Leu Lys
 85 90 95
 Tyr Leu Thr Glu Ala Val Leu Ser Arg Ile Gln Pro Gly Gly Ser Ile
 100 105 110
 Val Asn Val Ser Ser Val Leu Gly Ala Glu Trp Pro Ala Arg Leu Gln
 115 120 125
 Leu His Lys Glu Leu Gly Ser Val Val Gly Phe Ser Glu Gly Gln Ala
 130 135 140
 Trp Leu Lys Gln Asn Pro Val Ala Pro Glu Phe Cys Tyr Gln Tyr Phe
 145 150 155 160
 Lys Glu Ala Leu Ile Val Trp Ser Gln Val Gln Ala Gln Glu Trp Phe
 165 170 175
 Met Arg Thr Ser Val Arg Met Asn Cys Ile Ala Pro Gly Pro Val Phe
 180 185 190
 Thr Pro Ile Leu Asn Glu Phe Val Thr Met Leu Gly Gln Glu Arg Thr
 195 200 205
 Gln Ala Asp Ala His Arg Ile Lys Arg Pro Ala Tyr Ala Asp Glu Val
 210 215 220
 Ala Ala Val Ile Ala Phe Met Cys Ala Glu Glu Ser Arg Trp Ile Asn
 225 230 235 240

Gly Ile Asn Ile Pro Val Asp Gly Gly Leu Ala Ser Thr Tyr Val
245 250 255

<210> 43
<211> 26
<212> DNA
<213> Pseudomonas sp.

<400> 43
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<210> 44
<211> 20
<212> PRT
<213> Pseudomonas sp.

<220>
<221> UNSURE
<222> (12)

<220>
<221> UNSURE
<222> (13)..(19)

<400> 44
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1 5 10 15

Xaa Xaa Xaa Xaa
20

<210> 45
<211> 20
<212> PRT
<213> Pseudomonas sp.

<220>
<221> UNSURE
<222> (20)

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1 5 10 15

Ser Ala Leu Xaa
20